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2	1692.8	98.8	1785	6	AX747274	Sequence
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18	380.2	22.2	386	6	AX644346	Sequence

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DEFINITION Sequence 799 from Patent EP1308459.
ACCESSION AX747274
VERSION AX747274.1 GI:32131662
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Isoqai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1308459-A 799 07-MAY-2003;
Helix Research Institute (JP) ; Research Association for
Biotechnology (JP)
FEATURES
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ORIGIN

Query Match 98.8%; Score 1692.8; DB 6; Length 1785;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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TITLE	Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Sato, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T., and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs
PUBMED	Nat. Genet. 36 (1), 40-45 (2004)
REFERENCE	14702039
AUTHORS	2 Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K., and Isogai, T. NEDO human cDNA sequencing project
REFERENCE	Unpublished
AUTHORS	3 (bases 1 to 1785)
TITLE	Isogai, T. and Yamamoto, J. Direct Submission
JOURNAL	Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
COMMENT	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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Best Local Similarity	99.9%; Pred. No. 0;
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PUBMED
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AUTHORS
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BC033143
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Eukaryota
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Mammalia
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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2 (bases 1 to 1679)
NIH MGC Project
Direct Submission

JOURNAL
REMARK
COMMENT

Submitted (25-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
Contact: MGC help desk
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moka, Johnson
Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR
Santos, Duane Smalus, Jeff Stott, Miranda Tsai, George Yang,
Jacquie Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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LOCUS AX535029 1977 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 56 from Patent WO02068633.
ACCESSION AX535029
VERSION AX535029.1 GI:25261664
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
Compositions and methods relating to lung specific genes and
proteins
Patent: WO 02068633-A 56 06-SEP-2002;
Diadexus, Inc. (US)
Location/Qualifiers
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/db_xref="taxon:9606"

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Query Match 93.5%; Score 1602.4; DB 6; Length 1977;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 11; Gaps 9;
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RESULT 6
AX535090
LOCUS AX535090
DEFINITION Sequence 117 from Patent WO02068633.
ACCESSION AX535090
VERSION AX535090.1 GI:25261789
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Macina,R.A., Recipon,H., Chen,S.Y., Sun,Y., Sun,Y. and Liu,C.
TITLE Compositions and methods relating to lung specific genes and proteins
JOURNAL Patent: WO 02068633-A 117 06-SEP-2002;
Diadexus, Inc. (US)
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source 1..1977
Location/Qualifiers
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ORIGIN
Query Match 93.5%; Score 1602.4; DB 6; Length 1977;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 11; Gaps 9;

Qy 1 ATGCCCGCCCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACCGTGGAG 60
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Qy 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCCCAAGCCGC 120
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DEFINITION Sequence 3609 from Patent WO02068579.
ACCESSION CQ717675
VERSION CQ717675.1 GI:42278532
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominidae; Homo.
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REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 3609 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 4.1e-282;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AL356390
LOCUS
DEFINITION
Human DNA sequence from clone RP11-344H11 on chromosome 1. Contains
the NR0B2 gene for nuclear receptor subfamily 0 (group B, member
2), the 5' end of a novel gene (FLJ12455), the NUDC gene for nuclear
distribution gene C homolog (A. nidulans), a novel gene (FLJ34633),
a ribosomal protein l12 (RP112) pseudogene, a ribosomal protein l32
(RP132) pseudogene, a novel pseudogene (DC2), two novel genes and
two CpG islands, complete sequence.
ACCESSION
AL356390
VERSION
AL356390.24 GI:21436506
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KEYWORDS
SOURCE
ORGANISMHomo sapiens (human)
Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.REFERENCE
AUTHORS
TITLE
JOURNAL1 (bases 1 to 140207)
Glithero, R.
Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk

COMMENT

On Jun 17, 2002 this sequence version replaced gi:20218554.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RP11-344H11 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6

Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk

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mRNA

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Matches 1039; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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BC006890
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BC006890 1680 bp mRNA linear ROD 29-JUN-2004
Mus musculus RIKEN CDNA 1810019J16 gene, mRNA (CDNA clone MGC:11921
IMAGE:3599314), complete cds.
BC006890
BC006890.1 GI:13905189
MGC.
Mus musculus (house mouse)

REFERENCE
AUTHORS

1 (bases 1 to 1680)
Strausberg R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
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Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932

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JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 1680)
Strausberg,R.
Direct Submission
Submitted (27-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegod, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

REMARK
COMMENT

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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This clone was selected for full length sequencing because it
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FEATURES
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Sciurognathi; Muridae; Murinae; Rattus.				
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REFERENCE				
AUTHORS				
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Loquellano N.A., Peters G.J., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				


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Db 104729 AGCATCACGAGGACTACCACTGGATGAGCAAGACGCCGAGGCGCCTGGTGGCGGC 104788
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QY 901 ATCATTCGATAGTACCCGAAGACCGTGTGGCCCAAGACCTCGGAGGGTCTTTCA 960
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Db 104789 ATCATCCGTATTAGTACCCGCAAAACCGCTCCGCCCAAGACCTCCGAGGGGCGCTCA 104848
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QY 961 ACTCGGGCTGTGCCCAACCGCTGTGCCCTGACAGTGGCCATGAGACCATGTGGGC 1020
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Db 104849 GCCCGCTTACTGTGCC---CTGCTGTGCCCGCAGAGTGGCCATGAGACCATGTGGGC 104905
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QY 1021 TCAGGTCTTCAGCCAGGATG 1039
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Db 104906 TCTGGCCTCAGCCAGGACG 104924
|||||

RESULT 13
AC095979
LOCUS
DEFINITION
Rattus norvegicus clone CH230-11020, WORKING DRAFT SEQUENCE, 3
unordered pieces.
AC095979
VERSION
GI:24818145
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
KEYWORDS
Rattus norvegicus (Norway rat)
SOURCE
Rattus norvegicus
ORGANISM
Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Rattus.
1 (bases 1 to 235419)
Muzny,D,Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,P.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Caesar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escoto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hoques,M.,
Hollins,B., Howells,S., Hulvik,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokemele,O., Okuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Prankoch,C.,
Flopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steinle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villaseana,D., Waldron,L., Walker,B., Wang,J.,
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Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wlarczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,E., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 235419)
Worley,K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235419)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:22772470.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project information
Center project name: GEBU
Center clone name: CH230-11020
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 22536 bases at least Q40
Consensus quality: 227458 bases at least Q30
Consensus quality: 228649 bases at least Q20
Estimated insert size: 235033; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 221492: contig of 221492 bp in length
* 221493 221592: gap of unknown length
* 221593 228651: contig of 7059 bp in length
* 228652 228751: gap of unknown length
* 228752 235419: contig of 6668 bp in length.
* Location/Qualifiers
1. .235419
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-11020"
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misc_feature
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  end_sequence: BH344795"
  21911..220573
  /note="clone boundary
  clone end: Sp6
  site: EcoRI
  end_sequence: BH344813"
  221493..221592
  /estimated_length=unknown
  228652..228751
  /estimated_length=unknown

ORIGIN
Query Match      45.1%; Score 773.4; DB 14; Length 235419;
Best Local Similarity 84.7%; Pred. No. 2.2e-178;
Matches 880; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

QY 1 ATGCCCCGCTGAGACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACCGTGGAG 60
Db 83086 ATGCCAGCGGGAGACGCCCGCCCATGCTCTGGGCTCCAGCTTGGGGCCCTGGAG 83145
QY 61 CGGCCAACAGAGCTATGCTGGAGACATATGATAAACCACTCAGCCCCCACCACGCGC 120
Db 83146 AGCCCAACAGAGTTATGCTTGGAAACGAATGATGAGCGCTCCAGCCCCCACCAGCGCT 83205
QY 121 CGACCCGTTAGACAGACACCCACAGACCTTGGGCAACATGGGCGCAGAGCATTTACCTTC 180
Db 83206 CGACCCGTTAGAGACACCTTAAGGACCTTGGCCACACCGGCGCAGAGCATCACCTTC 83265
QY 181 ATCTCTGCTCTGCTGAGCGCGCTTGTAGTCTCCCACTGCTGCTCTGCTCTGCGGACCC 240
Db 83266 ATTTCAGCTCTGAGAACAGCAACGAGCCCGCCCACTGCTGCTCTGCGGCGCC 83325
QY 241 TGGGTGTGGAGTGTGCTGGGCTGCTCTTCTGCTTCCGCGCTGCGGAGTTCCTCCAG 300
Db 83326 TGGGTGTGGAGTGTGCTGGGCTGCTCTTCTGCTTCCGAGCTGCGAGGATGCTCCAG 83385
QY 301 CGCTGTGAGCCTGTGTGCGGAGATGACGCCCTGCTGCTTCTACTAGAGATCTCACTGAG 360
Db 83386 CGCTGTGAGCCTGTGTGCGGAGCTGTAGCCCTGCTTACTGCTGAGAGCCCATTTGA 83445
QY 361 GCGACTGCTGAAGCAACTGGGCCAGGAGCACAATGAGTGGTGGCCCGCCAGCCTGATCGT 420
Db 83446 GGGTCTTGGAGCGCTGCGGAGGATGGGCAAGCAACAGCGTGTGCTTCCAGCCAGACCGA 83505
QY 421 GCACCCCGCAGCGGGGATGCGCAGCGCTCAAGTCAACCATGGGCGAGCAGCTTCAGC 480
Db 83506 GCACCCCGCAGCGCGGATGGGCAAGCAACCTCAAGACAGCATGGGCGAGCAGCTTCAGC 83565
QY 481 TACCCCGATTTAAGCTCAAGGATCCCTGTGTATCCCTTACCGAGGGCCACCTCCCA 540
Db 83566 TACCTGTATTTAAGCTCAAGGATCCCTGTGTATCCCTTACCGAGGGCCACCTCCCA 83625
QY 541 GCCCTGTAGCGGACTCTGCTGAGGAGGAGCAGTGGCCGATCCCGCCAGCGAGCAGC 600
Db 83626 GTCCCTGTAGCGGACTCTGCTGAGGAGGAGCAGTGGCCGATCCCGCCAGCGAGCAGC 83685
QY 601 AGCTGCGCAGCAGCCTTTGCGAGTAGTCTGCTGGGCTCCGAGGAGTACTATTCTTTCCAT 660
Db 83686 AGCTGCGCAGCAGCCTTTGCGAGTAGTCTGCTGGGCTCCGAGGAGTACTATTCTTTCCAT 83745
QY 661 GAGTGGAGCTTGAACCTTCCGAGATGGGCGAGTGGCTTCCATGTCGAGCGGAGAAATGTAT 720
Db 83746 GAATGGAGCTTGAACCTTCCGAGATGGGCGAGTGGCTTCCATGTCGAGCGGAGATCGAC 83805
QY 721 GTGCTATCTTCAAGAGCTGACAGAGCTGTTGAGGTACACAGATCGATGAGCTGGCC 780
Db 83806 GTGCTATCTTCAAGAGCTGACAGAGCTGTTGAGGTACACAGATCGATGAGCTGGCC 83865
QY 781 AAGTGACATCAGACACTGTGTTCTTGGAGAACAGCAGTAAAGATCTCGGACCTTATCAGC 840
Db 83866 AAGTGACATCAGATACCGTGTCTTGGAGAAACAGCAGTAAAGATCTCAGACCTGATCAGC 83925
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Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wlezyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished

TITLE
JOURNAL
REFERENCE
2 (bases 1 to 249406)

Worley,K.C.
Direct Submission
Submitted (22-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE
3 (bases 1 to 249406)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT
On Nov 15, 2002 this sequence version replaced gi:23269749.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GVHY
Center clone name: CH230-180E4

----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 213357 bases at least Q40
Consensus quality: 215358 bases at least Q30
Consensus quality: 217213 bases at least Q20
Estimated insert size: 223109; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 249406: contig of 249406 bp in length.

FEATURES
source

1. 249406
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-180E4"

misc_feature
1. 1279
/note="wgs_contig"

ORIGIN

Query Match 45.1%; Score 773.4; DB 14; Length 249406;
Best Local Similarity 84.7%; Pred. No. 2.2e-178;

	Matches	880;	Conservative	0;	Mismatches	156;	Indels	3;	Gaps	1;
QY	1	ATGCCCGCCCTGGACACACCCCGCCAGCATCTGGGCTCCACGCTTGGAGCCGTGGGAG	60							
Db	14756	ATGCCAGGCGCGGACAGCCCGCCCATCTGCTGGGCTTCCAGCTTGGGGCCCTGGGAG	14697							
QY	61	CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACTCAGCCCCCACAAGCCGC	120							
Db	14696	AGGCCACAGAGTTATGCTGGAAACGAATGATAGCGCTCCAGCCCCCACCAGGCCGT	14637							
QY	121	CGCACCGTAGACAGACCCCAAGGACCTTGGCCACCATGGGCCAGAGACATTACCTTC	180							
Db	14636	CGCACCGGAGCCAGACCCCTAAGGACCTTGGCCACCATGGGCCAGAGACATCACCTTC	14577							
QY	181	ATCTCTGGCTCTGCTGAGCGGCGCTTGTAGTCCCCCACTGTGCTGTCTCTGGCGACCC	240							
Db	14576	ATTTCAGGCTCTGCAAGAACCAACGAGCCCCCAACTGTCTGCTCTCTTGGGGCCCC	14517							
QY	241	TGGGTGTGGGAGTGGTGGCGGCTGCTTCTGCTTTCGCGCGCTGCGGGATTGCTTCCAG	300							
Db	14516	TGGGGTTGGGACTGGTGTAGGGCTGCCITCTCTCCGACGCTGCAGGGATTGCCCTCAG	14457							
QY	301	CGCTGTGAGACCTGTGTGCGGGGATGAGCCCTCGCTGTCTACTGAGACTCCACTGAG	360							
Db	14456	CGCTGTGAGACTGTGTGCGGAGCTGTAGCCCTCTTATCTGTGAGAGACCCCATTTGAA	14397							
QY	361	GGGACTGTGAAGCCAACTGGGCCAAGGAGACAAATGAGTGCCGCCAGCCCTGATCGT	420							
Db	14396	GGGTCTTTCGAAGCCGCTTGGGCCAAGAAACAACAGGTGTGCTTCCAGCCAGACCA	14337							
QY	421	GCACCCCCCAGCGCGGGATGGCCAGCGGCTCAAGTCAACCATCGGACGAGCTTCAGC	480							
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QY	481	TACCCCGATGTTAAGCTCAAGGATTCCTGTGTATTCCTACCGAGGGCCACCTCCCA	540							
Db	14276	TACCTCGATGTTAAGCTCAAGGGCATTCGCGTCTACCCCTACCGCATCCACCTCC	14217							
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RESULT 15
AC126312/c
LOCUS
DEFINITION
AC126312 256017 bp DNA linear HTG 13-NOV-2002
Rattus norvegicus clone CH230-189, *** SEQUENCING IN PROGRESS ***,
3 unordered pieces.
AC126312
AC126312.4 GI:24941465
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.
1 (bases 1 to 256017)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, P.R., Allen, C.,
Alsbrooks, S.L., Amarantunga, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burck, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
DeLaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabieli, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, D.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseghe, H.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokwenkwo, S., Ogih, M., Okwionu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sodergren, E., Sonaika, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczek, R., Woodson, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 256017)
Worley, K.C.
Direct Submission
TITLE
Submitted (05-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 256017)
Worley, K.C.
Direct Submission
TITLE
Submitted (13-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:23267435.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas

(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: TUNU
Center clone name: CH230-189
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 214827 bases at least Q40
Consensus quality: 219116 bases at least Q30
Consensus quality: 221911 bases at least Q20
Estimated insert size: 222841; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 83721: contig of 83721 bp in length
* 83722 83821: gap of unknown length
* 83822 253567: contig of 169746 bp in length
* 253568 253667: gap of unknown length
* 253668 256017: contig of 2350 bp in length.

FEATURES

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/note="wgs contig"
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/estimated_length=unknown
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misc_feature
misc_feature
misc_feature
gap
misc_feature
misc_feature
gap

ORIGIN

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Matches 880; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

1 ATGCCCGCCCTGGACACACCCGCCGATCTGGGCTCCACGTTGGGACCGTGGAG 60

Job time : 8485 secs

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Db 154727 TCTGGCCTCAGCCAGGATG 154709
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 19:35:11 ; Search time 1063 Seconds
(without alignments)
10739.999 Million cell updates/sec

Title: US-09-989-890-105
Perfect score: 1713
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1713	100.0	1713	8 ABT13390	Abt13390 Breast sp
2	1694.6	98.9	2392	10 ADD01260	Add01260 Human nuc
3	1692.8	98.8	1785	10 ADB62645	Adb62645 Human cdn
4	1602.4	93.5	1977	6 ABX92075	Abx92075 Lung spec
5	1602.4	93.5	1977	6 ABX92014	Abx92014 Lung spec
6	763	44.5	791	14 AEA19545	Aea19545 Novel hum
7	607.6	35.5	654	6 ABT07645	Abt07645 Human bre
8	463.2	27.0	728	2 AAZ17414	Aaz17414 Human gen
9	385	22.5	385	6 ABX92013	Abx92013 Lung spec
10	380.2	22.2	386	6 ABT07644	Abt07644 Human bre
11	380.2	22.2	386	8 ABT13389	Abt13389 Breast sp
12	352.6	20.6	393	5 AAF64421	Aaf64421 Novel hum
13	347	20.3	427	5 AAF66376	Aaf66376 Novel hum
14	300	17.5	300	2 AAZ13392	Aaz13392 Human gen
15	298.4	17.4	300	2 AAX98308	Aax98308 Human can
16	120	7.0	120	6 ABX92074	Abx92074 Lung spec
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	24	43.6	2.5	346	2	AAX54724		Aax54724 Human GM-
	25	43.6	2.5	346	3	AAA34171		Aaa34171 Human ade
	26	43.6	2.5	346	3	AAF20293		Aaf20293 Human GM-
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	28	43.6	2.5	7033	3	AAF20844		Aaf20844 Human low
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C	38	43	2.5	2289	9	ACC59893		Acc59893 Human REM
C	39	43	2.5	2359	4	AAS28798		Aas28798 Human imm
C	40	43	2.5	2359	10	ADB31523		Adb31523 Human CDN
C	41	43	2.5	2370	4	ABA06478		Aba06478 Human CDN
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ALIGNMENTS

RESULT 1
ABT13390
ID ABT13390 standard; DNA; 1713 BP.

AC ABT13390;

DT 30-JAN-2003 (first entry)

DE Breast specific related polynucleotide SEQ ID No 105.

KW Cytostatic; BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer;
KW metastatic; breast cancer; breast specific; human; db.

OS Homo sapiens.

PN WO200277232-A2.

PD 03-OCT-2002.

XX 21-NOV-2001; 2001WO-US043815.

XX 22-NOV-2000; 2000US-0252509P.

XX (DIAD-) DIADEXUS INC.

XX Salceda S, Macina RA, Recipon H, Pluta J, Sun Y, Liu C;

XX WPI; 2003-018927/01.

PT New isolated nucleic acid molecule, useful for treating breast cancer,
PT and diagnosing or monitoring the presence of metastases of breast cancer
PT in a patient.

PS Claim 1; Page 250-251; 377pp; English.

CC The invention relates to a novel isolated nucleic acid molecule
CC comprising: a sequence encoding a sequence comprising 11-1518 amino acids
CC ; a sequence comprising 190-8144 bp; or a sequence that selectively
CC hybridizes to, or having at least 60% identity with the 11-1518 amino
CC acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are
CC useful for treating breast cancer, and diagnosing or monitoring the
CC presence of metastases of breast cancer in a patient. The polynucleotides

CC of the invention can be used to treat disorders by gene therapy. This
CC polynucleotide represents a breast specific related sequence of the
CC invention

XX	SQ	Sequence 1713 BP; 344 A; 553 C; 468 G; 348 T; 0 U; 0 Other;	
		Query Match 100.0%; Score 1713; DB 8; Length 1713;	
		Best Local Similarity 100.0%; Pred. No. 0;	
		Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB	1	ATGCCCGCCCTGGACACCCCGCCCGCAGCATCTGGGCTTCCAGCTTGGGACCGTGGGAG 60	
QY	61	CGGCCAACAGAGCTATGCTGGAGACATATGATAAACCACTCAGCCCCCCACCAAGCCGC 120	
DB	61	CGGCCAACAGAGCTATGCTGGAGACATATGATAAACCACTCAGCCCCCCACCAAGCCGC 120	
QY	121	CGCACCCGTAGACACAGCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCATTTACTTTC 180	
DB	121	CGCACCCGTAGACACAGCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCATTTACTTTC 180	
QY	181	ATCTCTGGCTTGTCTGAGCGCGCCCTTGGTTCCTCCACCTGTCTGCTCTGGCGACCC 240	
DB	181	ATCTCTGGCTTGTCTGAGCGCGCCCTTGGTTCCTCCACCTGTCTGCTCTGGCGACCC 240	
QY	241	TGGGTGTGGAGTGTGTGCGGGTGTCTTGTCTTGGTTCGGCGGTTCGGGATTCCTCCAG 300	
DB	241	TGGGTGTGGAGTGTGTGCGGGTGTCTTGTCTTGGTTCGGCGGTTCGGGATTCCTCCAG 300	
QY	301	CGCTGTGGAGCTGTCTGCGGGATGACGCCCTGTCTGTCTACTGAGACTCCACTGAG 360	
DB	301	CGCTGTGGAGCTGTGTGCGGGATGACGCCCTGTCTGTCTACTGAGACTCCACTGAG 360	
QY	361	GGGACTGTCTGAAGCCAACTGGGCCAAGGAGCAAAATGGAGTGCCCCCAGCCCTGATCGT 420	
DB	361	GGGACTGTCTGAAGCCAACTGGGCCAAGGAGCAAAATGGAGTGCCCCCAGCCCTGATCGT 420	
QY	421	GCACCCCGCAGCGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCGAGCAGCTTCAGC 480	
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QY	481	TACCCCGATGTTAAGCTCAAGGCATCCCTGTGTATCCCTTACCCGAGGGCCACTCCCCA 540	
DB	481	TACCCCGATGTTAAGCTCAAGGCATCCCTGTGTATCCCTTACCCGAGGGCCACTCCCCA 540	
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DB	601	AGCTGCCAGACACTTTGGCAGTAGTCTCTGTGGCTCCGAGGAGTACTATTCTTTCCAT 660	
QY	661	GAGTCGAGCTGACACTGCTCGGAGATGGGAGTGGCTCCATGTCGAGCGAGAAATGAT 720	
DB	661	GAGTCGAGCTGACACTGCTCGGAGATGGGAGTGGCTCCATGTCGAGCGAGAAATGAT 720	
QY	721	GTGCTCATCTTCAAGAGCTGACAGAGCTGTTTCAAGGTGACACAGATCGATGAGCTGGCC 780	
DB	721	GTGCTCATCTTCAAGAGCTGACAGAGCTGTTTCAAGGTGACACAGATCGATGAGCTGGCC 780	
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DB	781	AGTGACATCAGACATGTTGTTCTTGGAGAGAACCAAGTAAAGTCTCGGACCTTATCAGC 840	
QY	841	AGCATCAGCAGGACTACCACTGGATGACAGAGTCTGAGGGCGGCTGTGGTACGCGGC 900	
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QY	901	ATCATTCGCATTAGTATCCCGAAAGACCGGTGCTCGCCCAACAGACCTCGGAGGTCGTCA 960	
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DB	1081	ATGCCCCGAACTGAGGCTTATGGAGCTCAGGGTACCCAGAGCCATGACTCATCC 1140	
QY	1141	TTCCAGGGCACGACACAGACTCTGCGGGGACCCCTTCTCCAGGTGACTGCTAAACCC 1200	
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DB	1381	TCCTTGCACTCCCGAGCTGTCTGATCCCTGCGAGGCCCTTCTCTTCTGCTCATGGTCT 1440	
QY	1441	TCAGTGGGCTCATCATGGAAGTAAAGGATTTAGGCATTTACCTTCTGGAGTGAACCCCTG 1500	
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DB	1501	ACTCCATCCCTTATTTGCCACCTAACCAATCATGCAAACTTCTCCTCCTGGGGTAAT 1560	
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RESULT 2

ADD01260

ID ADD01260 standard; cDNA; 2392 BP.

XX AC ADD01260;

XX AC AC

DT 01-JAN-2004 (first entry)

XX

DE Human nucleic acid-associated protein NAAP-41 cDNA SEQ ID NO:98.

XX

XX

KW human; nucleic acid-associated protein; NAAP; cyostatic;

KW antiarteriosclerotic; anti-HIV; antiallergic; cerebroprotective;

KW antiparkinsonian; anticonvulsant; nootropic; neuroprotective;

KW antiinflammatory; ophthalmological; thyromimetic; antiarthritic;

KW hepatotropic; antibacterial; virucide; protozoacide; antiparasitic;

KW fungicide; gene therapy; cell proliferative disease; cancer;

KW atherosclerosis; hepatitis; neurological disorder; Parkinson's disease;

KW Alzheimer's disease; stroke; epilepsy; developmental disorder;

KW renal tubular acidosis; anaemia; glaucoma; hypothyroidism;

601 AGCTGCCAGCAGCTTTGCCAGTAGTCTCTGGTCCGAGGAGTACTATTCTTTCCAT 660
Db |||||
690 AGCTGCCAGCAGCTTTGCCAGTAGTCTCTGGTCCGAGGAGTACTATTCTTTCCAT 749
QY
661 GAGTCGAGCCTGACCTGCGGAGATGGGAGTGGTCTCCATGTCGAGCCGAGAAATGAT 720
Db |||||
750 GAGTCGAGCCTGACCTGCGGAGATGGGAGTGGTCTCCATGTCGAGCCGAGAAATGAT 809
QY
721 GTCTCATCTTCAAGAGCTGACAGAGCTTTACGGGTACACAGATCGATGAGCTGGCC 780
Db |||||
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QY
841 AGCATCAGCAGGACTACCACTGGATGAGCAGATGCTGAGGGCGGCTGTGACCGGC 900
Db |||||
930 AGCATCAGCAGGACTACCACTGGATGAGCAGATGCTGAGGGCGGCTGTGACCGGC 989
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901 ATCATTTGCAATTAGTACCCGAAAGAGCGTGTGCGCCACAGACCTCGGAGGGTCTGTCA 960
Db |||||
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QY
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1050 ACTCGGGCTGCTGCCCNACCGCTGTGCCCTGACAGTGGCCATGAGACCATGTTGGC 1109
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Db |||||
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Db |||||
1170 ATGCCCCGGAAGCTGAGGCGCTTATGAGGCTCCAGGGTACCCAGAACCATGACTCATCC 1229
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Db 1770 CACAGTTTGTAGTAC 1785

RESULT 4

ABX92075
ID ABX92075 standard; cDNA; 1977 BP.

XX ABX92075;

DT 08-MAY-2003 (first entry)

XX Lung specific nucleic acid (LSNA) #117.

XX Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
KW non-cancerous diseases of the lung; transgenic animal; gene; ss.

XX Homo sapiens.

XX WO200268633-A2.

XX 06-SEP-2002.

XX 21-NOV-2001; 2001WO-US043612.

XX 22-NOV-2000; 2000US-0252500P.

XX (DIAD-) DIADEXUS INC.

XX Macina RA, Recipon H, Chen S, Sun Y, Liu C;

XX WPI; 2002-713376/77.

XX New isolated human nucleic acid molecule and polypeptide, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating lung
PT cancer and non-cancerous diseases of the lung.

XX Claim 1; Page 266-267; 389pp; English.

XX The invention describes an isolated human nucleic acid (I) encoding any
CC of 120 10-1533 residue amino acid sequences (S1), given in the
CC specification, comprising any of 164 179-1241 base pair sequences (S2),
CC given in the specification. The methods and compositions of the present
CC invention are useful for identifying, diagnosing, monitoring, staging,
CC imaging and treating lung cancer and non-cancerous diseases of the lung.
CC They are also used for identifying lung tissue, monitoring and
CC identifying and/or designing antagonists of the polypeptide of the
CC invention, gene therapy, production of transgenic animals and production
CC of engineered lung tissue for treatment and research. This sequence
CC encodes a lung specific nucleic acid

XX Sequence 1977 BP; 393 A; 631 C; 554 G; 399 T; 0 U; 0 Other;

Query Match 93.5%; Score 1602.4; DB 6; Length 1977;

Best Local Similarity 99.0%; Pred. No. 0;

Matches 1707; Conservative 0; Mismatches 6; Indels 11; Gaps 9;

QY 1 ATGCCCGCCCTGGACACCCCGCCGAGCATCTGGGCTCCAGCTTGGACCGTGGAG 60

Db 254 ATGCCCGCCCTGGACACCCCGCCGAGCATCTGGGCTCCAGCTTGGACCGTGGAG 313

QY 61 CGGCCAACAGAGCATGTCTGGAGACATATGATAAACACACCTCAGCCCCCACCAGCCGC 120

Db 314 CGGCCAACAGAGCATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCAGCCGC 373

QY 121 CGCACCCGTAGACACCCCAAGGACCTGGCCACCATGGGCCAGAGCATTAACCTTC 180

Db 374 CGCACCCGTAGACACCCCAAGGACCTGGCCACCATGGGCCAGAGCATTAACCTTC 433

QY 181 ATCTCTGGCTCTGCTGAGCGGGCCCTTGTAGTCCCCCAGCTGCTGCTGGCGACCC 240

Db 434 ATCTCTGGCTCTGCTGAGCGGGCCCTTGTAGTCCCCCAGCTGCTGCTGGCGACCC 493

QY 241 TGGGTGTGGAGTGGTCCGGGCTGCTTCTGCTTCGG-CCGCTGCGCGGATTGCTCTCA 299
DB 494 TGGGTGTGGAGTGGTCCGGGCTGCTTCTGCTTCGGCCGCTGCGGGATTGCTCTCA 553
QY 300 GCGCTGTGGA-GCCTGTGTGCGGGGATGAGCCCTGCTGTCTACTAGGACT-CCACT 357
DB 554 GCGCTGTGAGGCCCTGTGTGCGGGATGAGCCCTGCTGTCTACTAGGACTTCCACT 613
QY 358 GAGGGACTGTGAGCCCAACTGG-GCCAAAGAGCAATGAGTGTCCCCCGAGCCCTGA 416
DB 614 GAGGGACTGTGAGCCCAACTGGTGCAGAGGACAAATGAGTGTCCCCCGAGCCCTGA 673
QY 417 TCGTGACACCCCGAG-CCGGCGGGATGGCCA--GGGGCTCAAGTCAACCAATGGGGAGCA 472
DB 674 TCGTGACACCCCGAGCCCGGGATGGCCAGCGGGCTGCAAGTCAACCAATGGGGAGCA 733
QY 473 GCTTCAGCTACCCCGATGTTAAGCTCAAAAGGATCCCTGTGTATCCCTACCCGAG-GGCC 531
DB 734 GCTTCAGCTACCCCGATGTTAAGCTCAAAAGGATCCCTGTGTATCCCTACCCGAGAGGCC 793
QY 532 ACCTCCCGAGCCCTGATCGGACTCTCTGCTGCAAGGAGCCACTGCGCGATCCCGACCC 591
DB 794 ACCTCCCGAGCCCTGATCGGACTCTCTGCTGCAAGGAGCCACTGCGCGATCCCGACCC 853
QY 592 ATGCGA-CACAGCTGCCAGCACCTTTGCCAGTAGTCTCTGCTGGCTCCGAGGAGTACTA 650
DB 854 ATGCGAGCACAGCTGCCAGCACCTTTGCCAGTAGTCTCTGCTGGCTCCGAGGAGTACTA 913
QY 651 TTCTTTCCATGATCGGACTCGGACTGCGCGAGATGGGAGTGGCTCCATGTCCAGCGC 710
DB 914 TTCTTTCCATGATCGGACTCGGACTGCGCGAGATGGGAGTGGCTCCATGTCCAGCGC 973
QY 711 AGAAATGATGTCTCATCTTCAAGAGCTGACAGA-GCTGTTACGGGTACACAGATCG 769
DB 974 AGAAATGATGTCTCATCTTCAAGAGCTGACAGAGGCTGTTACAGCGTACACAGATCG 1033
QY 770 ATGAGCTGCCAAGTGCATCAGACATCAGACATGTGTTCTCGAGAGAGCCAGTAAAGTCTCG 829
DB 1034 ATGAGCTGCCAAGTGCATCAGACATCAGACATGTGTTCTCGAGAGAGCCAGTAAAGTCTCG 1093
QY 830 ACCTTATCAGCAGCATCAGCAGGACTACACCTGGATGAGCAGGATGCTGAGGGCCGCC 889
DB 1094 ACCTTATCAGCAGCATCAGCAGGACTACACCTGGATGAGCAGGATGCTGAGGGCCGCC 1153
QY 890 TGGTACGGCGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTGCCCAACAGACCTCGG 949
DB 1154 TGGTACGGCGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTGCCCAACAGACCTCGG 1213
QY 950 AGGGTGGTTCAACTCGGGCTGTGCCCAACCGCTGCTGCCCTGACAGTGGCCATGACA 1009
DB 1214 AGGGTGGTTCAACTCGGGCTGTGCCCAACCGCTGCTGCCCTGACAGTGGCCATGACA 1273
QY 1010 CCATGGTGGGCTCAGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCAGGAGACGA 1069
DB 1274 CCATGGTGGGCTCAGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCAGGAGACGA 1333
QY 1070 CTGAGATGCCATTCGCCCGGAGCTGAGGCTTTATGGAGCTCCAGGGTACCAGCAAGCC 1129
DB 1334 CTGAGATGCCATTCGCCCGGAGCTGAGGCTTTATGGAGCTCCAGGGTACCAGCAAGCC 1393
QY 1130 ATGACTCATCTTCCAGGGCACCAGACAGACTCTGTCGGGGCACCCTTGTCTCCAGGTCT 1189
DB 1394 ATGACTCATCTTCCAGGGCACCAGACAGACTCTGTCGGGGCACCCTTGTCTCCAGGTCT 1453
QY 1190 ACTGTCAACCCCTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGCGCTTACAG 1249
DB 1454 ACTGTCAACCCCTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGCGCTTACAG 1513
QY 1250 ATGAAGAGGGGACAGAGAACCCCTGTGGGAGAGGCTTAGACCTGAACGATGCGCCACT 1309
DB 1514 AATGAAGAGGGGACAGAGAACCCCTGTGGGAGAGGCTTAGACCTGAACGATGCGCCACT 1573

QY 1310 CTGGCTCTCTCTGCTTGGCTGACTGGGTTCTGGACCATGTGCATTTCACTGGGCCATG 1369
DB 1574 CTGGCTCTCTCTGCTTGGCTGACTGGGTTCTGGACCATGTGCATTTCACTGGGCCATG 1633
QY 1370 GGATCTAATCTCTCTTGATGCCAGTCCCTGATCCCTGATCCCTGAGGGCCCTTCTTCTCT 1429
DB 1634 GGATCTAATCTCTCTTGATGCCAGTCCCTGATCCCTGATCCCTGAGGGCCCTTCTTCTCT 1693
QY 1430 GCTCATGGTCTTTCAGTGGCCCTGATCATGGAAGTAAAGAGTTAGGCATTTACTTCTGGG 1489
DB 1694 GCTCATGGTCTTTCAGTGGCCCTGATCATGGAAGTAAAGAGTTAGGCATTTACTTCTGGG 1753
QY 1490 AGTGAACCCCTGACTCCATCCCTTATGTCACCCCTTAAACCAATCATGCAAACTTCTCCCTC 1549
DB 1754 AGTGAACCCCTGACTCCATCCCTTATGTCACCCCTTAAACCAATCATGCAAACTTCTCCCTC 1813
QY 1550 CTGCGGGTAAATTCACAGTTAAAGAGCTTATCTTAAATGATTTGATTTGGGGGTGGG 1609
DB 1814 CTGCGGGTAAATTCACAGTTAAAGAGCTTATCTTAAATGATTTGATTTGGGGGTGGG 1873
QY 1610 CAGGGCCCACTCTATGTTATGTTAAGGAGTTGGTTCTGGTCTTGGCTGATGTTCTGTAT 1669
DB 1874 CAGGGCCCACTCTATGTTATGTTAAGGAGTTGGTTCTGGTCTTGGCTGATGTTCTGTAT 1933
QY 1670 CTTAAACATGACCACAGTTTGTAAAGTACCTCGGCCCGGACACGC 1713
DB 1934 CTTAAACATGACCACAGTTTGTAAAGTACCTCGGCCCGGACACGC 1977

RESULT 5
ABX92014

ID ABX92014 standard; cdna; 1977 BP.

XX AC ABX92014;

XX DT 08-MAY-2003 (first entry)

XX Lung specific nucleic acid (LSNA) #56.

DE Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
KW non-cancerous diseases of the lung; transgenic animal; gene; ss.

XX OS Homo sapiens.

XX PN WO200268633-A2.

XX PD 06-SEP-2002.

XX PF 21-NOV-2001; 2001WO-US043612.

XX PR 22-NOV-2000; 2000US-0252500P.

XX (DIAD-) DIADEXUS INC.

XX PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;

XX DR WPI; 2002-713376/77.

XX New isolated human nucleic acid molecule and polypeptide, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating lung
PT cancer and non-cancerous diseases of the lung.

XX PS Claim 1; Page 205-206; 389pp; English.

XX The invention describes an isolated human nucleic acid (I) encoding any
CC of 120 10-1533 residue amino acid sequences (S1), given in the
CC specification, comprising any of 164 179-12421 base pair sequences (S2),
CC given in the specification. The methods and compositions of the present
CC invention are useful for identifying, diagnosing, monitoring, staging,
CC imaging and treating lung cancer and non-cancerous diseases of the lung.
CC They are also used for identifying lung tissue, monitoring and
CC identifying and/or designing antagonists of the polypeptide of the

KW cytostatic; neoplasm; gene; ss.
XX Homo sapiens.
OS WO2005049806-A2.
XX 02-JUN-2005.
XX 11-MAR-2004; 2004WO-US007412.
XX 14-MAR-2003; 2003US-00389559.
XX (NUVE-) NUVELO INC.
XX Tang TY, Wang J, Wang ZW, Zhang J, Ren F, Zhou P, Ma Y;
PI Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R;
PI Wehrman T, Weng G, Boyle B;
XX WPI; 2005-417730/42.
DR P-PSDB; AEA20112.
XX
XX New polynucleotide encoding a polypeptide with biological activity,
PT useful for treating a disease or disorder, e.g. osteoarthritis, burns,
PT CNS and peripheral disease, stroke, autoimmune disorders, viral
PT infection, or cancer.
XX
XX Claim 1; SEQ ID NO 239; 500pp; English.
XX
XX The invention describes a new isolated polynucleotide (I) encoding a
CC polypeptide with biological activity comprising: a nucleotide sequence of
CC SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes
CC to the sequence of (I) under stringent hybridization conditions; or a
CC nucleotide sequence having greater than 9% sequence identity with the
CC sequence of (I). Also described are: a(n) (expression)vector comprising
CC (I); a host cell genetically engineered to comprise (I) operatively,
CC associated with a regulatory sequence that modulates expression of the
CC polynucleotide in the host cell; an isolated polypeptide comprising a
CC sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide
CC is a polypeptide encoded by (I); or a polypeptide encoded by a
CC polynucleotide hybridizing under stringent conditions with any one of SEQ
CC ID NOS: 1-567; a composition comprising the polypeptide of (3) and a
CC carrier; an antibody directed against the polypeptide of (3); a method
CC for detecting (I) in a sample; a method for detecting the polypeptide of
CC (3) in a sample; a method for identifying a compound that binds to the
CC polypeptide of (3); a method of producing the polypeptide of (3); and a
CC collection of polynucleotides, where the collection comprising of at
CC least one of SEQ ID NOS: 1-567. (I) is a polynucleotide comprising any of
CC the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological
CC activity, which comprises any of the amino acid sequence of SEQ ID NOS:
CC 568-1134. All sequences are fully defined in the specification. The
CC sequences and methods are useful in diagnostics, forensic, and gene
CC mapping, in identifying of mutations responsible for genetic disorders or
CC other traits, in assessing biodiversity, and for producing many other
CC types of data and products dependent on DNA and amino acid sequences. The
CC composition and method are useful for treating a disease or disorder,
CC e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and
CC peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,
CC autoimmune disorders, viral infection, or cancer. This sequence encodes a
XX novel polypeptide of the invention.
XX
XX Sequence 791 BP; 149 A; 278 C; 222 G; 142 T; 0 U; 0 Other;
Query Match 44.5%; Score 763; DB 14; Length 791;
Best Local Similarity 99.7%; Pred. No. 7.1e-196;
Matches 785; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 1 ATGCCCGCCCTGGACACCCCGCCGAGCATCTGGGCTCCACGCTTGGGACCGTGGGAG 60
DB 1 ATGCCCGCCCTGGACACCCCGCCGAGCATCTGGGCTCCACGCTTGGGACCGTGGGAG 60
QY 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAAACCACTCAGCCCCCAACAGCCGC 120
DB 61 CGG-CAACAGAGCTATGTCTGGAGACATATGATAAAACCACTCAGCCCCCAACAGCCGC 119

QY 121 CGCACCCGTAGACCAGACCCCAAGGACCCCTGGCCACCATGGGCCAGAGAGCATTTACCTTC 180
DB 120 CGCACCCGTAGACCAGACCCCAAGGACCCCTGGCCACCATGGGCCAGAGAGCATTTACCTTC 179
QY 181 ATCTCTGGCTCTGCTGAGCCCGCCCTTGTAGTCCCCACACCTGCTGCTGCTGCGGACCC 240
DB 180 ATCTCTGGCTCTGCTGAGCCCGCCCTTGTAGTCCCCACACCTGCTGCTGCTGCGGACCC 239
QY 241 TGGGTGTGGAGTGTGTGCGGGCTGCTTCTGCTTCCGCGCTGCGGGATTTGCCCTCCAG 300
DB 240 TGGGTGTGGAGTGTGTGCGGGCTGCTTCTGCTTCCGCGCTGCGGGATTTGCCCTCCAG 299
QY 301 CGCTGTGGAGCTGTGTGCGGGATGCGAGCCCTGCTCTCTACTGAGGACTCCACTGAG 360
DB 300 CGCTGTGGAGCTGTGTGCGGGATGCGAGCCCTGCTCTCTACTGAGGACTCCACTGAG 359
QY 361 GGGACTGCTGAAGCCAACTGGGCCCAAGGAGCAATGGAGTGCCCCCAGCCCTGATCGT 420
DB 360 GGGACTGCTGAAGCCAACTGGGCCCAAGGAGCAATGGAGTGCCCCCAGCCCTGATCGT 419
QY 421 GCACCCCCAGCCGGGGATGGCCAGCGGCTCAAGTCAACCATGGGCGAGGACTTCAGC 480
DB 420 GCACCCCCAGCCGGGGATGGCCAGCGGCTCAAGTCAACCATGGGCGAGGACTTCAGC 479
QY 481 TACCCCGATGTTAAGCTCAAGGCGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA 540
DB 480 TACCCCGATGTTAAGCTCAAGGCGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA 539
QY 541 GCCCTGTATGCGGACTCTGTGTCGAAGGAGCCACTGGCCGATCCCCCACCCTATGCGACAC 600
DB 540 GCCCTGTATGCGGACTCTGTGTCGAAGGAGCCACTGGCCGATCCCCCACCCTATGCGACAC 599
QY 601 AGCCTGCCAGACACCTTTGCCAGTAGTCTCTGCTGCTCGAGGAGTACTATTCTTTCCAT 660
DB 600 AGCCTGCCAGACACCTTTGCCAGTAGTCTCTGCTGCTCGAGGAGTACTATTCTTTCCAT 659
QY 661 GAGTGGGACCTGGACCTGCGCGAGATGGGAGTGCGCTCCATGTCGAGCCGAGAAATTGAT 720
DB 660 GAGTGGGACCTGGACCTGCGCGAGATGGGAGTGCGCTCCATGTCGAGCCGAGAAATTGAT 719
QY 721 GTGCTCATCTTCAAGAAGCTGACAGA-GCTGTTAGCGGTACACCATCGATGAGTGGC 779
DB 720 GTGCTCATCTTCAAGAAGCTGACAGAGGCTGTTACGCGTACACCATCGATGAGTGGC 779
QY 780 CAAGTGC 786
DB 780 CAAGTGC 786
RESULT 7
ABT07645
ID ABT07645 standard; cDNA; 654 BP.
XX
AC ABT07645;
XX
DT 14-NOV-2002 (first entry)
XX
DE Human breast cancer associated coding sequence SEQ ID NO: 124.
XX
KW Human; breast specific gene; breast specific protein; breast cancer;
KW gene therapy; cytostatic; gene; ss.
OS Homo sapiens.
XX WO200264611-A1.
XX 22-AUG-2002.
XX 12-FEB-2002; 2002WO-US004197.
XX 13-FEB-2001; 2001US-0268292P.
XX

PA (DIAD-) DIADEXUS INC.
XX Salceda S, Macina RA, Hu P, Recipon H, Karra K, Caferkey R;
PI Sun Y, Liu C;
XX WPI; 2002-657582/70.
XX New breast specific nucleic acids and proteins, useful for identifying,
PT diagnosing, monitoring, staging, imaging, and treating breast cancer and
PT non-cancerous disease states in breast tissue, and in gene therapy.
XX
XX Claim 1; Page 248; 367pp; English.
XX
XX The present invention provides human breast specific coding sequences and
CC proteins. These can be used in the diagnosis and treatment of breast
CC cancer and non-cancerous diseases of the breast. The present sequence is
CC a coding sequence of the invention
XX
XX Sequence 654 BP; 118 A; 232 C; 186 G; 118 T; 0 U; 0 Other;
SQ
Query Match 35.5%; Score 607.6; DB 6; Length 654;
Best Local Similarity 96.6%; Pred. No. 7.8e-154;
Matches 632; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
WPI; 1999-494092/41.
QY 89 ATGATAACCACTCAGCCGCCCCCAGCAGCCGCGCCGCTAGACGAGACCCAGGACC 148
DB 1 ATGATAACCACTCAGCCGCCCCCAGCAGCCGCGCCGCTAGACGAGACCCAGGACC 60
QY 149 CTGGCCACCACTGGCCGAGAGATTAATCTTCACTCTGGCTCTGAGCGGCCCTTG 208
DB 61 CTGGCCACCACTGGCCGAGAGATTAATCTTCACTCTGGCTCTGAGCGGCCCTTG 120
QY 209 AGTCCCCCACTGCTGCTCTCTGGCGACCCCTGGGTGTGGAGTGTGCGGCTGCT 268
DB 121 AGTCCCCCACTGCTGCTCTCTGGCGACCCCTGGGTGTGGAGTGTGCGGCTGCT 180
QY 269 TCTGCTTCGCGCTGCGCGATGCTCTCCAGCGCTGTGAGCGCTGTGCGGGATGCA 328
DB 181 TCTGCTTCGCGCTGCGCGATGCTCTCCAGCGCTGTGAGCGCGTGTGCGGGATGCA 240
QY 329 GCCCTCCCTGTCTACTGAGGACTTCCACTGAGGGGAGTGTGAGCCAACTGGGCCAAG 388
DB 241 GCCCTCCCTGTCTACTGAGGACTTCCCTGAGGGGAGTGTGAGCCAACTGTGTCGAAG 300
QY 389 AGCACAATGAGTGGCCGCCCCCAGCCCTGATGTGCAACCCCGCCGCGGATGGCCA-- 446
DB 301 AGCACAATGAGTGGCCGCCCCCAGCCCTGATGTGCAACCCCGCCGCGGATGGCCA 360
QY 447 -GGGCTCAAGTCAACATGGGAGGAGCTTCACTACCCCGATGTTAAGCTCAAGGCA 505
DB 361 CGGCTGCAAGTCAACATGGGAGGAGCTTCACTACCCCGATGTTAAGCTCAAGGCA 420
QY 506 TCCTGTGTATCCCTACCCGAGGCGCCACCTCCCGAGCCCTGATGCGGACTCTGCTGCA 565
DB 421 TCCTGTGTATCCCTACCCGAGGCGCCACCTCCCGAGCCCTGATGCGGACTCTGCTGCA 480
QY 566 AGGAGCCACTGGCCGATGCCGCCACCCACGACAGCCCTGCCAGACCTTTGCCAGTA 625
DB 481 AGGAGCCACTGGCCGATGCCGCCACCCACGACAGCCCTGCCAGACCTTTGCCAGTA 540
QY 626 GTCTCTGTGCTCGGAGGATCTATTCTTTTCCATGATGCGGACCTGGAACCTGCGGAGA 685
DB 541 GTCTCTGTGCTCGGAGGATCTATTCTTTTCCATGATGCGGACCTGGAACCTGCGGAGA 600
QY 586 TGGGCACTGCTCCATCTCGGCGGAGAAATGATGCTCATCTTCAAGAAC 739
DB 601 TGGGCACTGCTCCATCTCGGCGGAGAAATGATGCTCATCTTCAAGAAC 654
RESULT 8
AAZ17414
ID AAZ17414 standard; cDNA; 728 BP.
XX

AC AAZ17414;
XX 12-OCT-1999 (first entry)
XX Human gene expression product cDNA sequence SEQ ID NO:4887.
DE
XX Human; gene; gene expression product; diagnosis; therapy; probe;
KW detection; mapping; tissue typing; profiling; forensic; cancer;
KW genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX Homo sapiens.
XX WO9939972-A2.
XX 05-AUG-1999.
XX 28-JAN-1999; 99WO-US001619.
XX 28-JAN-1998; 98US-0072910P.
PR 24-FEB-1998; 98US-0075954P.
PR 31-MAR-1998; 98US-0080114P.
PR 03-APR-1998; 98US-0080515P.
PR 03-APR-1998; 98US-0080666P.
PR 21-OCT-1998; 98US-0105234P.
PR 28-OCT-1998; 98US-0105877P.
XX (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX Williams LT, Escobedo J, Inniss MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Glese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX WPI; 1999-494092/41.
XX Novel human genes and their expression products which are differentially
PT expressed in different cell types.
PT
XX Claim 1; Page 2323-2324; 2479pp; English.
XX The present invention describes a library of human polynucleotides
CC comprising the sequences given in AAZ12532 to AAZ17779. Also described is
CC a method of detecting differentially expressed genes correlated with the
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample from a cell
CC suspected of being cancerous, where the gene product is encoded by one of
CC the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The
CC polynucleotides can be used as a source of primers and probes, which can
CC be used for a variety of purpose, e.g. detection of expression levels,
CC mapping, tissue typing or profiling, forensics, genetic analysis and
CC detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC can be used for raising antibodies for experimental, diagnostic and
CC therapeutic purposes. The polynucleotides may also be used to construct
CC arrays for diagnostics (which may be used to determine function of an
CC encoded protein); and to detect differences in expression levels between
CC two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC identify a genetic predisposition or susceptibility to a disease such as
CC cancer). The polynucleotides of the invention are especially used in the
CC diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC and lung cancer. The polynucleotides can also be used to screen for
CC peptide analogues and antagonists
SQ Sequence 728 BP; 145 A; 190 C; 178 G; 150 T; 0 U; 65 Other;
Query Match 27.0%; Score 463.2; DB 2; Length 728;
Best Local Similarity 88.4%; Pred. No. 1e-114;
Matches 569; Conservative 0; Mismatches 66; Indels 9; Gaps 8;
QY 822 GATCTCGGACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGA 881
DB 91 GAGCTCGACCTTATNAGCAGCATNAGCATGACTACCACTGATNAGCAGGATGCTGA 150

QY 882 GGGCCCGTGGTACGGGATCATTCGCATTAGTACCAGAAAGACCGTGTCTGCCACCA 941
DB |||||
151 GGGCCCGTGGTACGGTGGATCATTCNATTAGTNCCTGGAAAGACCGTGTGGGNACA 210
QY 942 GACCTCGGAGGGTGGTTCAACTCGGCTGTCTGCCCAACCGTGTCTGCCCTTGACAGTGG 1001
DB |||||
211 GA-CTCCGAGGGTGGTTCAACT-NGGCTGTGTCTCCCAACCGTGTCTGACCTTGACAGTGG 268
QY 1002 CCATGAGACCATGGTGGGTCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCA 1061
DB |||||
269 CCATGANACCATGGGGGTCTCAGGTCTTACTCAGNATGAGCTGACAGTGCANATCTCCNA 328
QY 1062 GGAGACCACTGACAGATGCCATCCCGGAACTGAGGCGCTTATGAGAGCTCCAGGGTACCC 1121
DB |||||
329 GGAGACCACTGACAGATGCCATCCCGGAACTGAGGCGCTTATGAGAGCTCCAGGGTACCC 388
QY 1122 AGC-AAGCCATGACTCATCTCTCCAGGGCAACGACACAGACTCGTC-GGGGGCACCTTTG 1179
DB |||||
389 AGCAAGCCATGACTCATCTCTTCANGGCAACGACACAGACTCGTCTGGGGGCACCTTTG 448
QY 1180 CTCCAGGTGACTGCTTAACCTCTGCCAGCCAGCTGCCACACCTTTCTGGGAGAGCA 1239
DB |||||
449 CTNCAAGTGTACTGATAACNCNTGACAGGCCCATCTGGCACACCTTTCTGGGAGAGCA 508
QY 1240 TGGCCTACAGATGAAGAGGGGACAGGAACCCCTGTGGGAGAGCTTAGACCTGAAGC 1299
DB |||||
509 TGGCCTACAGATGAAGAGGGGACAGGAACCCCTGTGGGAGAGCTTAGACCTGAAGC 1359
QY 1300 AGTGGCCACTCTGGCTCCTCTCTGCTTGGCTGACTGGGTTCCTGGACCAATGTGCAATTCA 1359
DB |||||
568 AGTGGCCACTCTGGTCTCTGCTTGGCTGACTGGTTCCTGGACCAATGTGCAATTCA 626
QY 1360 CTGGGCACTGGGATCATCATCTCTTGCATCCCGAGCTGTGTGATCCCTGCCAGGGGCC 1419
DB |||||
627 CTGGNCACTGGGATCATCATCT-CTTGCATNCCANCTGG--CTGATCTCTGCCANGGCC 683
QY 1420 CTTCCTCTCTGCTCATGTCTTCAGGTGGCTCATCATGGAAG 1463
DB |||||
684 GTTNCNTCTGCTCATGNCNTTGNNGNCTGATCATNGAAG 727

RESULT 9

ABX92013
ID ABX92013 standard; cDNA; 385 BP.

AC ABX92013;

XX 08-MAY-2003 (first entry)

XX Lung specific nucleic acid (LSNA) #55.

XX Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
KW non-cancerous diseases of the lung; transgenic animal; gene; ss.

XX Homo sapiens.

XX WO200268633-A2.

XX 06-SEP-2002.

XX 21-NOV-2001; 2001WO-US043612.

XX 22-NOV-2000; 2000US-0252500P.

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CC imaging and treating lung cancer and non-cancerous diseases of the lung.
CC They are also used for identifying lung tissue, monitoring and
CC identifying and/or designing antagonists of the polypeptide of the
CC invention, gene therapy, production of transgenic animals and production
CC of engineered lung tissue for treatment and research. This sequence
CC encodes a lung specific nucleic acid

XX Sequence 385 BP; 80 A; 122 C; 93 G; 90 T; 0 U; 0 Other;

QY Query Match 22.5%; Score 385; DB 6; Length 385;

Best Local Similarity 100.0%; Pred. No. 1.2e-93;

Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 ACTGCTAAACCTTGCAGGCCAGCTGCCACACCTTTCTGGGAGAGCATGGCCTTACAG 60
DB |||||

QY 1250 AATGAGAGGGGACCGAAGACCCCTGTGGGAGAGCTTAGACCTGAAGCAGTGGCCACT 1309
DB |||||

DB 61 AATGAGAGGGGACCGAAGACCCCTGTGGGAGAGCTTAGACCTGAAGCAGTGGCCACT 120
QY 1310 CTGGCTCTCTCTGCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTTCACTGGGCCATG 1369
DB |||||

DB 121 CTGGCTCTCTCTGCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTTCACTGGGCCATG 180
QY 1370 GGATCTACATCTCTTGCATCCCGAGCTGGTCTGATCCCTGCCAGGGCCCTTCTCTTCT 1429
DB |||||

DB 181 GGATCTACATCTCTTGCATCCCGAGCTGGTCTGATCCCTGCCAGGGCCCTTCTCTTCT 240
QY 1430 GCTCATGTGCTTTCAGGTGGCTGATCATGGAAGTAAGAGATTAGGCATTACCTCTGGG 1489
DB |||||

DB 241 GCTCATGTGCTTTCAGGTGGCTGATCATGGAAGTAAGAGATTAGGCATTACCTCTGGG 300
QY 1490 AGTGAACCTCTGACTCCATCCCTTATTCACCCCTTAACCAATCATGCAAACTTCTCCCTC 1549
DB |||||

DB 301 AGTGAACCTCTGACTCCATCCCTTATTCACCCCTTAACCAATCATGCAAACTTCTCCCTC 360
QY 1550 CTGGGGTAAATCAACAGTTAAAG 1574
DB |||||

DB 361 CCTGGGGTAAATCAACAGTTAAAG 385

RESULT 10

ABT07644

ID ABT07644 standard; cDNA; 386 BP.

XX AC ABT07644;

XX 14-NOV-2002 (first entry)

XX Human breast cancer associated coding sequence SEQ ID NO: 123.

XX Human; breast specific gene; breast specific protein; breast cancer;
KW gene therapy; cytostatic; gene; ss.

XX Homo sapiens.

XX WO200264611-A1.

XX 22-AUG-2002.

XX 12-FEB-2002; 2002WO-US004197.

XX 13-FEB-2001; 2001US-0268292P.

XX (DIAD-) DIADEXUS INC.
PA Salceda S, Macina RA, Hu P, Recipon H, Karra K, Cafferkey R;
PI Sun Y, Liu C;
XX WPI; 2002-657582/70.
XX New breast specific nucleic acids and proteins, useful for identifying,
PT diagnosing, monitoring, staging, imaging, and treating breast cancer and
PT non-cancerous disease states in breast tissue, and in gene therapy.
XX Claim 1; Page 248; 367pp; English.
XX The present invention provides human breast specific coding sequences and
CC proteins. These can be used in the diagnosis and treatment of breast
CC cancer and non-cancerous diseases of the breast. The present sequence is
CC a coding sequence of the invention
XX
SQ Sequence 386 BP; 81 A; 121 C; 94 G; 90 T; 0 U; 0 Other;
Query Match 22.2%; Score 380.2; DB 6; Length 386;
Best Local Similarity 99.2%; Pred. No. 2.3e-92;
Matches 382; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1196 AACCCCTGCGAGCCAGCTGCCACACCCCTTCTGGGAGAGGCTTAGACCTGAGCAGTGGCCATGGAATGAA 1255
Db 2 ACCCCTGGCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGGCTTAGACCTGAGCAGTGGCCATGGAATGAA 61
QY 1256 GAGGGGGACAGAACCCCTGTTGGGAGAGGCTTAGACCTGAGCAGTGGCCATGGAATGAA 1315
Db 62 GAGGGGGACAGAACCCCTGTTGGGAGAGGCTTAGACCTGAGCAGTGGCCATGGAATGAA 121
QY 1316 CCTCTGCTTGGCTGACTGGGTTCCTGGACCATGTGCAATTCACCTGGGCCATGGGATCT 1375
Db 122 CCTCTGCTTGGCTGACTGGGTTCCTGGACCATGTGCAATTCACCTGGGCCATGGGATCT 181
QY 1376 ACATCTCCTTGCATCCCGAGCTGGTCTGATCCTCGCAGGCCCCCTTCTCTCTGCTCAT 1435
Db 182 ACATCTCCTTGCATCCCGAGCTGGTCTGATCCTCGCAGGCCCCCTTCTCTCTGCTCAT 241
QY 1436 GGTCTTCAGTGGCCCTGATCATGGAAGTAAGAGTATAGGCATTACCTCTGGGAGTGAA 1495
Db 242 GGTCTTCAGTGGCCCTGATCATGGAAGTAAGAGTATAGGCATTACCTCTGGGAGTGAA 301
QY 1496 CCTGACTCCATCCCTTATGCGACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGG 1555
Db 302 CCTGACTCCATCCCTTATGCGACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGG 361
QY 1556 GTAAATTCACAGTTAAAGAAGCTT 1580
Db 362 GTAAATTCACAGTTAAAGAAGCTT 386
RESULT 12
ABT13389
ID ABT13389 standard; DNA; 386 BP.
XX ABT13389;
XX
XX
DT 30-JAN-2003 (first entry)
XX Breast specific related polynucleotide SEQ ID No 104.
DE
DE Cytostatic; BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer;
KW metastatic; breast cancer; breast specific; human; ds.
XX Homo sapiens.
OS
PN WO200277232-A2.
XX
PD 03-OCT-2002.
XX

PF 21-NOV-2001; 2001WO-US043815.
XX
PR 22-NOV-2000; 2000US-0252509P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Salceda S, Macina RA, Recipon H, Pluta J, Sun Y, Liu C;
XX WPI; 2003-018927/01.
XX
XX New isolated nucleic acid molecule, useful for treating breast cancer,
PT and diagnosing or monitoring the presence of metastases of breast cancer
PT in a patient.
XX
XX Claim 1; Page 250; 377pp; English.
XX The invention relates to a novel isolated nucleic acid molecule
CC comprising: a sequence encoding a sequence comprising 11-1518 amino acids
CC ; a sequence comprising 190-8144 bp; or a sequence that selectively
CC hybridizes to, or having at least 60% identity with the 11-1518 amino
CC acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are
CC useful for treating breast cancer, and diagnosing or monitoring the
CC presence of metastases of breast cancer in a patient. The polynucleotides
CC of the invention can be used to treat disorders by gene therapy. This
CC polynucleotide represents a breast specific related sequence of the
CC invention
XX
SQ Sequence 386 BP; 81 A; 121 C; 94 G; 90 T; 0 U; 0 Other;
Query Match 22.2%; Score 380.2; DB 8; Length 386;
Best Local Similarity 99.2%; Pred. No. 2.3e-92;
Matches 382; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1196 AACCCCTGCGAGCCAGCTGCCACACCCCTTCTGGGAGAGGCTTAGACCTGAGCAGTGGCCATGGAATGAA 1255
Db 2 ACCCCTGGCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGGCTTAGACCTGAGCAGTGGCCATGGAATGAA 61
QY 1256 GAGGGGGACAGAACCCCTGTTGGGAGAGGCTTAGACCTGAGCAGTGGCCATGGAATGAA 1315
Db 62 GAGGGGGACAGAACCCCTGTTGGGAGAGGCTTAGACCTGAGCAGTGGCCATGGAATGAA 121
QY 1316 CCTCTGCTTGGCTGACTGGGTTCCTGGACCATGTGCAATTCACCTGGGCCATGGGATCT 1375
Db 122 CCTCTGCTTGGCTGACTGGGTTCCTGGACCATGTGCAATTCACCTGGGCCATGGGATCT 181
QY 1376 ACATCTCCTTGCATCCCGAGCTGGTCTGATCCTCGCAGGCCCCCTTCTCTCTGCTCAT 1435
Db 182 ACATCTCCTTGCATCCCGAGCTGGTCTGATCCTCGCAGGCCCCCTTCTCTCTGCTCAT 241
QY 1436 GGTCTTCAGTGGCCCTGATCATGGAAGTAAGAGTATAGGCATTACCTCTGGGAGTGAA 1495
Db 242 GGTCTTCAGTGGCCCTGATCATGGAAGTAAGAGTATAGGCATTACCTCTGGGAGTGAA 301
QY 1496 CCTGACTCCATCCCTTATGCGACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGG 1555
Db 302 CCTGACTCCATCCCTTATGCGACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGG 361
QY 1556 GTAAATTCACAGTTAAAGAAGCTT 1580
Db 362 GTAAATTCACAGTTAAAGAAGCTT 386
RESULT 12
AAF64421
ID AAF64421 standard; cDNA; 393 BP.
XX AAF64421;
XX
XX
DT 09-APR-2001 (first entry)
XX Novel human polynucleotide, SEQ ID NO: 177.
DE Human; cytostatic; gene therapy; colon cancer; prostate cancer;
XX

```
KW breast cancer; lung cancer; cancer detection; ss.
XX Homo sapiens.
XX WO200102568-A2.
XX 11-JAN-2001.
XX 30-JUN-2000; 2000WO-US018374.
XX 02-JUL-1999; 99US-0142310P.
XX 02-JUL-1999; 99US-0142311P.
XX (CHIR ) CHIRON CORP.
XX (HYSE-) HYSEQ INC.
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Klingler J;
PI Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G;
PI Drmanac R, Crkenjakov R, Drmanac S, Dickson M, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Strache-Crain B;
XX WPI; 2001-091805/10.
XX Library of polynucleotides for diagnosing a cancerous state of a
PT mammalian cell and detecting cancer, particularly of the colon or
PT prostate, comprises 3351 human polynucleotide sequences.
XX Claim 9; Page 570; 1046pp; English.
XX The present sequence is one of 3351 sequences in a library of human
CC polynucleotides. The library is used to detect differentially expressed
CC genes correlated with a cancerous state of a mammalian cell and can
CC detect colon, prostate, breast and lung cancer. The library can be used
CC to produce probes for detection of mRNA and to produce additional copies
CC of the polynucleotides. The probes can be used for chromosome mapping of
CC the polynucleotide and for detection of transcription levels. Ribozymes
CC or antisense oligonucleotides can be generated. The polynucleotides and
CC their gene products are used as genetic or biochemical markers (e.g. in
CC blood or tissues) that will detect the earliest changes along the
CC carcinogenesis pathway and/or monitor the efficacy of therapies and
CC preventive interventions. The polynucleotides, polypeptides and
CC antibodies against them can be used in pharmaceutical compositions to
CC treat the cancers and proliferative disorders such as neoplasia,
CC dysplasia and hyperplasia
XX Sequence 393 BP; 88 A; 122 C; 115 G; 67 T; 0 U; 1 Other;
Query Match 20.6%; Score 352.6; DB 5; Length 393;
Best Local Similarity 98.4%; Pred. No. 7e-85;
Matches 366; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 805 CTGGAGAAGACGAGTGAAGTCTCGGACCTTATCAGCAGCATACGCGAGCTACGACCTG 864
DB 21 CTGGAGAAGACGAGTGAAGTCTCGGACCTTATCAGCAGCATACGCGAGCTACGACCTG 80
QY 865 GATGACGAGTGTCTGAGGCGCCCTGCTACGGGCTATTCGCGGCTAGTACCGAAG 924
DB 81 GATGACGAGTGTCTGAGGCGCCCTGCTACGGGCTATTCGCGGCTAGTACCGAAG 140
QY 925 AGCGGTGCTCGCCACAGACCTCGGAGGGTCTGTTCAACTCGGCTGCTGCCCCAACCGCT 984
DB 141 AGCGGTGCTCGCCACAGACCTCGGAGGGTCTGTTCAACTCGGCTGCTGCCCCAACCGCT 200
QY 985 GTGCCCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGTTCTAGCCAGATGAGCTG 1044
DB 201 GCTGCCCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGTTCTAGCCAGATGAGCTG 260
QY 1045 ACAGTGCAGATCTCCAGGAGACGACTGCAGATGCCATGCCCGGAGCTGAGGCTTAT 1104
DB 261 ACAGTGCAGATCTCCAGGAGACGACTGCAGATGCCATGCCCGGAGCTGAGGCTTAT 320
QY 1105 GGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCTTCCA -GGGCACCGACACAGACTC 1163
DB 1105 GGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCTTCCA -GGGCACCGACACAGACTC 1163
DB breast cancer; lung cancer; cancer detection; ss.
XX Homo sapiens.
XX WO200102568-A2.
XX 11-JAN-2001.
XX 30-JUN-2000; 2000WO-US018374.
XX 02-JUL-1999; 99US-0142310P.
XX 02-JUL-1999; 99US-0142311P.
XX (CHIR ) CHIRON CORP.
XX (HYSE-) HYSEQ INC.
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Klingler J;
PI Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G;
PI Drmanac R, Crkenjakov R, Drmanac S, Dickson M, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Strache-Crain B;
XX WPI; 2001-091805/10.
XX Library of polynucleotides for diagnosing a cancerous state of a
PT mammalian cell and detecting cancer, particularly of the colon or
PT prostate, comprises 3351 human polynucleotide sequences.
XX Claim 9; Page 570; 1046pp; English.
XX The present sequence is one of 3351 sequences in a library of human
CC polynucleotides. The library is used to detect differentially expressed
CC genes correlated with a cancerous state of a mammalian cell and can
CC detect colon, prostate, breast and lung cancer. The library can be used
CC to produce probes for detection of mRNA and to produce additional copies
CC of the polynucleotides. The probes can be used for chromosome mapping of
CC the polynucleotide and for detection of transcription levels. Ribozymes
CC or antisense oligonucleotides can be generated. The polynucleotides and
CC their gene products are used as genetic or biochemical markers (e.g. in
CC blood or tissues) that will detect the earliest changes along the
CC carcinogenesis pathway and/or monitor the efficacy of therapies and
CC preventive interventions. The polynucleotides, polypeptides and
CC antibodies against them can be used in pharmaceutical compositions to
CC treat the cancers and proliferative disorders such as neoplasia,
CC dysplasia and hyperplasia
XX Sequence 393 BP; 88 A; 122 C; 115 G; 67 T; 0 U; 1 Other;
Query Match 20.6%; Score 352.6; DB 5; Length 393;
Best Local Similarity 98.4%; Pred. No. 7e-85;
Matches 366; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 805 CTGGAGAAGACGAGTGAAGTCTCGGACCTTATCAGCAGCATACGCGAGCTACGACCTG 864
DB 21 CTGGAGAAGACGAGTGAAGTCTCGGACCTTATCAGCAGCATACGCGAGCTACGACCTG 80
QY 865 GATGACGAGTGTCTGAGGCGCCCTGCTACGGGCTATTCGCGGCTAGTACCGAAG 924
DB 81 GATGACGAGTGTCTGAGGCGCCCTGCTACGGGCTATTCGCGGCTAGTACCGAAG 140
QY 925 AGCGGTGCTCGCCACAGACCTCGGAGGGTCTGTTCAACTCGGCTGCTGCCCCAACCGCT 984
DB 141 AGCGGTGCTCGCCACAGACCTCGGAGGGTCTGTTCAACTCGGCTGCTGCCCCAACCGCT 200
QY 985 GTGCCCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGTTCTAGCCAGATGAGCTG 1044
DB 201 GCTGCCCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGTTCTAGCCAGATGAGCTG 260
QY 1045 ACAGTGCAGATCTCCAGGAGACGACTGCAGATGCCATGCCCGGAGCTGAGGCTTAT 1104
DB 261 ACAGTGCAGATCTCCAGGAGACGACTGCAGATGCCATGCCCGGAGCTGAGGCTTAT 320
QY 1105 GGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCTTCCA -GGGCACCGACACAGACTC 1163
DB 1105 GGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCTTCCA -GGGCACCGACACAGACTC 1163
DB breast cancer; lung cancer; cancer detection; ss.
XX Homo sapiens.
XX WO200102568-A2.
XX 11-JAN-2001.
XX 30-JUN-2000; 2000WO-US018374.
XX 02-JUL-1999; 99US-0142310P.
XX 02-JUL-1999; 99US-0142311P.
XX (CHIR ) CHIRON CORP.
XX (HYSE-) HYSEQ INC.
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Klingler J;
PI Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G;
PI Drmanac R, Crkenjakov R, Drmanac S, Dickson M, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Strache-Crain B;
XX WPI; 2001-091805/10.
XX Library of polynucleotides for diagnosing a cancerous state of a
PT mammalian cell and detecting cancer, particularly of the colon or
PT prostate, comprises 3351 human polynucleotide sequences.
XX Claim 9; Page 570; 1046pp; English.
XX The present sequence is one of 3351 sequences in a library of human
CC polynucleotides. The library is used to detect differentially expressed
CC genes correlated with a cancerous state of a mammalian cell and can
CC detect colon, prostate, breast and lung cancer. The library can be used
CC to produce probes for detection of mRNA and to produce additional copies
CC of the polynucleotides. The probes can be used for chromosome mapping of
CC the polynucleotide and for detection of transcription levels. Ribozymes
CC or antisense oligonucleotides can be generated. The polynucleotides and
CC their gene products are used as genetic or biochemical markers (e.g. in
CC blood or tissues) that will detect the earliest changes along the
CC carcinogenesis pathway and/or monitor the efficacy of therapies and
CC preventive interventions. The polynucleotides, polypeptides and
CC antibodies against them can be used in pharmaceutical compositions to
CC treat the cancers and proliferative disorders such as neoplasia,
CC dysplasia and hyperplasia
XX Sequence 427 BP; 69 A; 161 C; 123 G; 73 T; 0 U; 1 Other;
Query Match 20.3%; Score 347; DB 5; Length 427;
Best Local Similarity 99.7%; Pred. No. 2.4e-83;
Matches 347; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCCCCCGCTGGACACCCCGCCCGCCAGCATCTGGGCTCCAGCTTGGACCGTGGAG 60
DB 80 ATGCCCCCGCTGGACACCCCGCCCGCCAGCATCTGGGCTCCAGCTTGGACCGTGGAG 139
```

QY 61 CGGCCACAGAGCTATCTGGAGACATATGATTAACCACTCAGCCGCCACCAAGCGC 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
140 CGGCCACAGAGCTATCTGGAGACATATGATTAACCACTCAGCCGCCACCAAGCGC 199
QY 121 CGCACCCGTAGACAGACCCCAAGGACCCTGGCCACCATGGCCAGAGAGCATTAACCTTC 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
200 CGCACCCGTAGACAGACCCCAAGGACCCTGGCCACCATGGCCAGAGAGCATTAACCTTC 259
QY 181 ATCTCTGGCTCTGCTAGAGCGGCCCTTTGAGTCCCCACCTGCTGCTGCTGCGACCC 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
260 ATCTCTGGCTCTGCTAGAGCGGCCCTTTGAGTCCCCACCTGCTGCTGCTGCGACCC 319
QY 241 TGGGTGTGGGAGTGGTCCGGGCTGCTTCTGCTTCCGGCTGCTCCGGATTCCTCCAG 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
320 TGGGTGTGGGAGTGGTCCGGGCTGCTTCTGCTTCCGGCTGCTCCGGATTCCTCCAG 379
QY 301 CGCTGTGGAGCTGTGTGGGAGTGCAGCCCTGCTGCTACTGAG 348
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
380 CGCTGTGGAGCTGTGTGGGAGTGCAGCCCTGCTGCTACTGAG 427

RESULT 14

AAZ13392
ID AAZ13392 standard; cDNA; 300 BP.

XX AAZ13392;

AC
DT 12-OCT-1999 (first entry)

XX Human gene expression product cDNA sequence SEQ ID NO:861.

XX Human; gene; gene expression product; diagnosis; therapy; probe;

KW detection; mapping; tissue typing; profiling; forensic; cancer;

KW genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.

XX Homo sapiens.

XX WO9938972-A2.

XX 05-AUG-1999.

XX 28-JAN-1999; 99WO-US001619.

XX 28-JAN-1998; 98US-0072910P.

PR 24-FEB-1998; 98US-0075954P.

PR 31-MAR-1998; 98US-0080114P.

PR 03-APR-1998; 98US-0080515P.

PR 03-APR-1998; 98US-0080666P.

PR 21-OCT-1998; 98US-0105234P.

PR 28-OCT-1998; 98US-0105877P.

XX (CHIR) CHIRON CORP.

PA (HYSE-) HYSEQ INC.

XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;

PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;

PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;

PI Leschowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;

XX WPI; 1999-494092/41.

XX Novel human genes and their expression products which are differentially
PT expressed in different cell types.

XX Claim 1; Page 860; 2479pp; English.

XX The present invention describes a library of human polynucleotides
CC comprising the sequences given in AAZ12532 to AAZ17779. Also described is
CC a method of detecting differentially expressed genes correlated with the
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample from a cell
CC suspected of being cancerous, where the gene product is encoded by one of
CC the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The

CC polynucleotides can be used as a source of primers and probes, which can
CC be used for a variety of purpose, e.g. detection of expression levels,
CC mapping, tissue typing or profiling, forensic, genetic analysis and
CC detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC can be used for raising antibodies for experimental, diagnostic and
CC therapeutic purposes. The polynucleotides may also be used to construct
CC arrays for diagnostics (which may be used to determine function of an
CC encoded protein); and to detect differences in expression levels between
CC two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC identify a genetic predisposition or susceptibility to a disease such as
CC cancer). The polynucleotides of the invention are especially used in the
CC diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC and lung cancer. The polynucleotides can also be used to screen for
CC peptide analogues and antagonists

SQ Sequence 300 BP; 63 A; 96 C; 90 G; 51 T; 0 U; 0 Other;

Query Match 17.5%; Score 300; DB 2; Length 300;

Best Local Similarity 100.0%; Pred. No. 1.1e-70;

Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 825 CTCGACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGG 884

DB 1 CTCGACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGG 60

QY 885 CCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAGAGCGTGTGCCCCACAGAC 944

DB 61 CCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAGAGCGTGTGCCCCACAGAC 120

QY 945 CTCGGAGGCTGTTCACTCGGGCTGCTGCCCAACCGCTGCTGCCCTGACAGTGCCCA 1004

DB 121 CTCGGAGGCTGTTCACTCGGGCTGCTGCCCAACCGCTGCTGCCCTGACAGTGCCCA 180

QY 1005 TGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGTGCACAGTGAGATCTCCACAGGA 1064

DB 181 TGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGTGCACAGTGAGATCTCCACAGGA 240

QY 1065 GACGACTGACAGATGCCATGCCCGGAGCTGAGGCGCTTATGGAGCTCCAGGGTACCAGC 1124

DB 241 GACGACTGACAGATGCCATGCCCGGAGCTGAGGCGCTTATGGAGCTCCAGGGTACCAGC 300

RESULT 15

AAZ98308

ID AAZ98308 standard; cDNA; 300 BP.

XX AAZ98308;

XX 24-SEP-1999 (first entry)

XX Human cancer cell derived cDNA #34.

XX Cancer; human; colon; breast; lung; transmembrane receptor; ATPase;
KW integral membrane protein; aspartyl protease; GATA family; wnt family;
KW transcription factor; G-protein alpha subunit; protein phosphatase;
KW phospholipase binding protein; diacylglycerol binding protein; trypsin;
KW protein kinase; tyrosine phosphatase; developmental signalling protein;
KW WWP domain; therapy; forensic; genetic mapping; diagnostic;
KW detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
KW Wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
KW leukemia; lymphoma; dysplasia; hyperplasia; endometrium; adrenal;
KW prostate; ss.

XX Homo sapiens.

XX WO9933982-A2.

XX 08-JUL-1999.

XX 22-DEC-1998; 98WO-US027610.

XX 23-DEC-1997; 97US-0068755P.

PR 03-APR-1998; 98US-0080664P.

PR 21-OCT-1998; 98US-0105234P.
PR 27-OCT-1998; 98US-0105877P.
XX 21-DEC-1998; 98US-00217471.
XX (CHIR) HIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Glese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamon G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
XX
DR WPI; 1999-430243/36.
XX
XX
PT New isolated human polynucleotides.
XX
XX
PS Claim 1; Page 326; 591pp; English.
XX
CC This invention describes novel isolated human polynucleotides obtained by
CC screening for differential expression in colon cancer, breast cancer and
CC lung cancer cell lines. The polynucleotides of the invention are
CC represented in AA98275-X99118 and encode polypeptides of protein
CC families selected from 4 transmembrane segments integral membrane
CC proteins, 7 transmembrane receptors, ATPases associated with various
CC cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
CC transcription factors, G-protein alpha subunit, phorbolesters or
CC diacylglycerol binding proteins, protein kinase, protein phosphatase 2C,
CC protein tyrosine phosphatase, trypsin, wnt family of developmental
CC signalling proteins and WW/ezps/WWP domain containing proteins. The
CC encoded polypeptides also have a functional domain selected from Ank
CC repeat, basic region plus leucine zipper transcription factors,
CC bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger
CC (C2H2 type), zinc finger (CCHC class), and zinc-binding metalloprotease
CC domain. The polynucleotides encode polypeptides with similarity to known
CC protein families and are predicted to have similar properties. The novel
CC polynucleotides can be used to develop products for use as therapeutic
CC agents and in forensics, genetic analysis, mapping and diagnostic
CC applications. In particular, the product can be used for the detection
CC and management of cancers. They can be used for treating e.g. cervical
CC cancers, melanomas, colorectal adenocarcinomas, Wilm's tumour, sarcomas,
CC retinoblastoma, myosarcomas, lung carcinomas, leukemias, such as chronic
CC myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and
CC myeloid leukemia, and lymphomas such as histiocytic lymphoma, anhydric
CC hereditary ectodermal dysplasia, congenital alveolar dysplasia, and
CC epithelial dysplasia of the cervix, fibrous dysplasia of bone, and
CC mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
CC prostate or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of
CC the skin
XX
SQ Sequence 300 BP; 68 A; 90 C; 86 G; 56 T; 0 U; 0 Other;

Query Match 17.4%; Score 298.4; DB 2; Length 300;
Best Local Similarity 99.7%; Pred. No. 3e-70;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TCACAGAGCTGTTACGCGTACACAGATCGATGAGTGGCCCAAGTCACATCAGACACTG 799
DB 1 TCACAGAGCTGTTACGCGTACACAGATCGATGAGTGGCCCAAGTCACATCAGACACTG 60
QY 800 TGTTCCTGGAGAGACAGTACAGATCTCGGACCTTATCAGCAGCATCAGCAGGACTACC 859
DB 61 TGTTCCTGGAGAGACAGTACAGATCTCGGACCTTATCAGCAGCATCAGCAGGACTACC 120
QY 860 ACTGATGAGCAGGATGCTGAGGGCGCGCTGTGTACGCGGCATCATTCGATTTATGATACC 919
DB 121 ACTGATGAGCAGGATGCTGAGGGCGCGCTGTGTACGCGGCATCATTCGATTTATGATACC 180
QY 920 GAAGAGCGTGTCTCGCCACACAGACCTCGAGGGTGTCTCACTCGGGGTGTCGCCCAA 979
DB 181 GAAGAGCGTGTCTCGCCACACAGACCTCGAGGGTGTCTCACTCGGGGTGTCGCCCAA 240
QY 980 CGGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGTCTCAGCCAGGATG 1039

Db 241 CGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGTCTCAGCCAGGATG 300
Search completed: March 12, 2006, 04:23:06
Job time : 1066 secs

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OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 19:52:41 ; Search time 6305 Seconds
(without alignments)
12711.542 Million cell updates/sec

Title: US-09-989-890-105
Perfect score: 1713
Sequence: 1 atgccccgcctggacaccc.....taactggcgccgacacgc 1713

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1:	gb_est1:*
2:	gb_est2:*
3:	gb_est3:*
4:	gb_hic:*
5:	gb_est4:*
6:	gb_est5:*
7:	gb_est6:*
8:	gb_est7:*
9:	gb_gss1:*
10:	gb_gss2:*
11:	gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1451.2	84.7	1671	4	CR749558	CR749558 Homo sapi
2	1197	69.9	1197	11	DQ045548	DQ045548 Homo sapi
3	1145	66.8	1181	11	DQ045549	DQ045549 Pan trogl
4	951.8	55.6	1657	4	AK007551	AK007551 Mus muscu
5	803.6	46.9	975	3	BM460277	BM460277 AGENCOURT
6	791	46.2	1596	4	AK051860	AK051860 Mus muscu
7	731.4	42.7	753	7	CN289134	CN289134 170005999
8	687	40.1	917	5	BQ691555	BQ691555 AGENCOURT
9	679.6	39.7	1009	5	BY070606	BY070606 BX707606
10	669.4	39.1	1015	2	BE741035	BE741035 601594018
11	647	37.8	966	2	BE901537	BE901537 601677420
12	622	36.3	622	3	BM823479	BM823479 K-EST0094
13	577.8	33.7	582	3	BP315176	BP315176 BP315176
14	576.2	33.6	826	3	BI694617	BI694617 603347838
15	540.2	31.5	583	3	BP331524	BP331524 BP331524
16	526.6	30.7	556	1	AA573775	AA573775 nk07d10.8
17	510	29.8	510	1	AA316608	AA316608 EST188290
18	496.4	29.0	783	7	CK478920	CK478920 AGENCOURT
19	489.2	28.6	984	2	BF135747	BF135747 601781110
20	480.2	28.0	489	1	AI925416	AI925416 w030802.x
21	476	27.8	1040	3	BI411303	BI411303 602964692
22	470.6	27.5	680	3	BI653517	BI653517 603300520

23	469.2	27.4	677	10	AG071555	AG071555 Pan trogl
24	459.2	26.8	537	2	BF191474	BF191474 MA
25	455.8	26.6	513	6	CD702656	CD702656 EST19181
26	450.2	26.3	470	5	BX110746	BX110746 BX110746
27	441.8	25.8	825	8	DN936585	DN936585 AGENCOURT
28	441.6	25.8	944	3	BI905189	BI905189 603167516
29	410.6	24.0	746	3	BI905713	BI905713 603166180
30	410	23.9	535	5	BQ566109	BQ566109 G152a07.Y
31	406	23.7	930	3	BI413848	BI413848 602991514
32	402	23.5	423	1	AW008047	AW008047 wv48h06.x
33	395.6	23.1	623	2	BE741110	BE741110 601593919
34	394	23.0	586	2	BG082830	BG082830 H3081C02-
35	394	23.0	756	2	BG871324	BG871324 602792482
36	389.2	22.7	763	10	AG603040	AG603040 Mus muscu
37	384.2	22.4	609	2	BE533148	BE533148 601235445
38	381.8	22.3	918	2	BF144315	BF144315 601787134
39	375	21.9	412	1	AI216202	AI216202 qm37e07.x
40	370	21.6	370	1	AW589267	AW589267 xe27g07.x
41	363.2	21.2	769	7	CK473171	CK473171 AGENCOURT
42	355	20.7	722	3	BI409054	BI409054 602961119
43	345.6	20.2	488	1	AI669760	AI669760 tui2h08.x
44	345.2	20.2	738	2	BI078885	BI078885 602873115
45	341.2	19.9	491	1	AA856355	AA856355 vw99g12.x

ALIGNMENTS

RESULT 1
LOCUS CR749558 1671 bp mRNA linear HTC 19-AUG-2004
DEFINITION Homo sapiens mRNA; cDNA DKFZp686B17277 (from clone DKFZp686B17277).
ACCESSION CR749558
VERSION CR749558.1 GI:51476784
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1671)
AUTHORS Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Weil, B., Amid, C., Oeinger, A., Fobo, G., Han, M. and Wiemann, S.
CONSRMT The German cDNA Consortium
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing Consortium of the German Genome Project. This clone (DKFZp686B17277) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686B17277
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686B17277"
/tissue_type="prostate"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
/note="hypothetical protein, differentially spliced"
1..1671
/gene="DKFZp686B17277"
69..692
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/codon_start=1
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/db_xref="GI:51476785"
/translation="MPRPGRHPASGPPRLGPWERTLCLETYDKPPPPSRRTTR
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PPAGMAGSSGSPWMAASATPMLSSKASLCIPTRGPPOPLMRTTAAARHWDIPHPCD
TACPAPLPVVLVAPRSTILMSRSTWTCRRWAVAPCRABKLMCSSRS"

ORIGIN

Query Match 84.7%; Score 1451.2; DB 4; Length 1671;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1581; Conservative 0; Mismatches 3; Indels 118; Gaps 1;
1 ATGCCCCGCCCTGGACACCCGCCCGCCAGCATCTGGGCTCCACCGCTTGGAGCGGTGGAG 60
69 ATGCCCCGCCCTGGACACCCGCCCGCCAGCATCTGGGCTCCACCGCTTGGAGCGGTGGAG 128
61 CGGCCCAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCACCAAGCCGC 120
129 CGGCCCAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCACCAAGCCGC 188
121 CGCACCCGTAGACAGACACCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCAATTACTTTC 180
189 CGCACCCGTAGACAGACACCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCAATTACTTTC 248
181 ATCTCTGGCTCTGCTGAGCGGCCCTTGTAGTCCCCACCTGCTGCTGCTCTTGGCGACCC 240
249 ATCTCTGGCTCTGCTGAGCGGCCCTTGTAGTCCCCCA----- 285
241 TGGGTGTGGAGTGTGTGCGGGCTGCTTCTGTCTCGCGCTGCGCGGATGTCCTCCAG 300
286 ----- 285
301 CGCTGTGAGCCTGTGTGCGGGATGACGCCCTGCTCTACTAGAGACTCCACTGAG 360
286 -----CCTGTCTACTGAGGACTCCACTGAG 310
361 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACATGGAGTGCCCCCGCCAGCCCTGATCT 420
311 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACATGGAGTGCCCCCGCCAGCCCTGATCT 370
421 GCACCCCCCAGCGCGGGATGGCCAGCGGCTCAAGTCAACATGGGCGAGCAGCTTCAGC 480
371 GCACCCCCCAGCGCGGGATGGCCAGCGGCTCAAGTCAACATGGGCGAGCAGCTTCAGC 430
481 TACCCCGATGTTAAGCTCAAAAGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCA 540
431 TACCCCGATGTTAAGCTCAAAAGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCA 490
541 GCCCTGATGCGGACTCTGCTGCAAGGAGCCACTGGCCGATCCCGCCGATCCCGCCATGCGAC 600
491 GCCCTGATGCGGACTCTGCTGCAAGGAGCCACTGGCCGATCCCGCCGATCCCGCCATGCGAC 550
601 AGCCTGCCAGACACCTTTCAGTAGTCTCTGCTGGCTCCGAGGAGTACTATTCTTTCCAT 660
551 AGCCTGCCAGACACCTTTCAGTAGTCTCTGCTGGCTCCGAGGAGTACTATTCTTTCCAT 610
661 GAGTCCGACCTGGAACCTGCGGAGATGGGAGTGGCTCCATGTCGAGCGGAGAAATGTAT 720
611 GAGTCCGACCTGGAACCTGCGGAGATGGGAGTGGCTCCATGTCGAGCGGAGAAATGTAT 670
721 GTGCTCATCTTCAGAGAGCTGACAGAGCTGTTTTCAGGCTACACAGATCGATGAGCTGGCC 780
671 GTGCTCATCTTCAGAGAGCTGACAGAGCTGTTTTCAGGCTACACAGATCGATGAGCTGGCC 730
781 AAGTGACATCAGACACTGTGTTCTCGGAGAACAGCAGTAAGATCTCGACCTTATCAGC 840
731 AAGTGACATCAGACACTGTGTTCTCGGAGAACAGCAGTAAGATCTCGACCTTATCAGC 790
841 AGCATCAGCAGGACTACCACTCTGGATGACAGGATGCTGAGGGCGCGCTGTGTACCGGC 900
791 AGCATCAGCAGGACTACCACTCTGGATGACAGGATGCTGAGGGCGCGCTGTGTACCGGC 850

QY 901 ATCATTTCGATTAGTACCCGAAAGAGCGTGTGCTCGCCACAGACCTTCGAGGGTTCGTTCA 960
DB 851 ATCATTTCGATTAGTACCCGAAAGAGCGTGTGCTCGCCACAGACCTTCGAGGGTTCGTTCA 910
QY 961 ACTCGGGCTGTGCCCCCAACCGCTGTGCTGCTGACAGTGGCCATAGACCAATGTGGGC 1020
DB 911 ACTCGGGCTGTGCCCCCAACCGCTGTGCTGCTGACAGTGGCCATAGACCAATGTGGGC 970
QY 1021 TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGATGCC 1080
DB 971 TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGATGCC 1030
QY 1081 ATCGCCCGGAAGCTCAGGCGCTTATGAGCTCCAGGTTACCCAGCAAGCCACTGACTCATCC 1140
DB 1031 ATCGCCCGGAAGCTCAGGCGCTTATGAGCTCCAGGTTACCCAGCAAGCCACTGACTCATCC 1090
QY 1141 TTCCAGGGCACCCGACACAGACTCGTGGGGGACCCCTTGTCTCCAGGTGTACTGTAAACC 1200
DB 1091 TTCCAGGGCACCCGACACAGACTCGTGGGGGACCCCTTGTCTCCAGGTGTACTGTAAACC 1150
QY 1201 CTGCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGCGCTACAGAAAGAGGG 1260
DB 1151 CTGCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGCGCTACAGAAAGAGGG 1210
QY 1261 GGACCAAGGAAACCCCTGTGGGAGAGCTTAGACTGGAAGCAGTCCCACTCTGGCTCCTCC 1320
DB 1211 GGACCAAGGAAACCCCTGTGGGAGAGCTTAGACTGGAAGCAGTCCCACTCTGGCTCCTCC 1270
QY 1321 TGCTTGGCTGACTGGGTTCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 1380
DB 1271 TGCTTGGCTGACTGGGTTCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 1330
QY 1381 TCCTTGATCCCGAGTGTGTGATCCCTGCCAGGGCCCTTCTCTCTGCTCATGGTCT 1440
DB 1331 TCCTTGATCCCGAGTGTGTGATCCCTGCCAGGGCCCTTCTCTCTGCTCATGGTCT 1390
QY 1441 TCAGTGGCTCATCATGGAAGTAAAGGATTTAGGCATTTACCTTCTGGGAGTGAAACCTG 1500
DB 1391 TCAGTGGCTCATCATGGAAGTAAAGGATTTAGGCATTTACCTTCTGGGAGTGAAACCTG 1450
QY 1501 ACTCCATCCCCCTATTGCCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAA 1560
DB 1451 ACTCCATCCCCCTATTGCCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAA 1510
QY 1561 TCACAGTTTAAAGAGCTTATCTTAAATGTATTTGTTGGGGGTGGGAGGGCCCACT 1620
DB 1511 TCACAGTTTAAAGAGCTTATCTTAAATGTATTTGTTGGGGGTGGGAGGGCCCACT 1570
QY 1621 CTATGTATTTAAAGAGTGTGTTCTGTTCTGTTGCTGATGTTCTGTATCTTAAACATGAC 1680
DB 1571 CTATGTATTTAAAGAGTGTGTTCTGTTCTGTTGCTGATGTTCTGTATCTTAAACATGAC 1630
QY 1681 CACAGTTTGAAGTACCTCGC 1702
DB 1631 CACAGTTTGAAGTACAAAGGC 1652

RESULT 2
DQ045548
LOCUS
DEFINITION
Homo sapiens FLJ34633 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
DQ045548
VERSION
DQ045548.1
GI:66896763
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 1197)
AUTHORS
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,

601	AGCTGCCCGACACCTTTGCCAGTAGTCTCTGTGGCTCCGAGGAGTACTATTCTTTCCAT	660
661	GAGTCGGAGCTGGACCTGCGGAGATGGGACGTGGCTCCATGTCGAGCGGAGAAATTGAT	720
661	GAGTCGGAGCTGGACCTGCGGAGATGGGACGTGGCTCCATGTCGAGCGGAGAAATTGAT	720
721	GTGCTCATTTTCAAGAAGCTGACAGAGCTGTTTCAGGCTACACAGATCGATGAGTGCGCC	780
721	GTGCTCATTTTCAAGAAGCTGACAGAGCTGTTTCAGGCTACACAGATCGATGAGTGCGCC	780
781	AGTGCACATCAGACACTGCTGTTCTTGGAGAGACCACTAGATCTCCGACCTTATCAGC	840
781	AGTGCACATCAGACACTGCTGTTCTTGGAGAGACCACTAGATCTCCGACCTTATCAGC	840
841	AGCATCACGAGGACTTACCACCTGGATGAGCAGGATGCTGAGGGCGGCTGATCGCGCC	900
841	AGCATCACGAGGACTTACCACCTGGATGAGCAGGATGCTGAGGGCGGCTGATCGCGCC	900
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901	ATCATTTGCAATTAGTACCCGAAAGACCGTGTCTGCCACACAGACCTCGGAGGGTCTTCA	960
961	ACTCGGGCTGCTGCCACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGCTGGGCG	1020
961	ACTCGGGCTGCTGCCACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGCTGGGCG	1020
1021	TCAGGTCTCAGCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGATGCC	1080
1021	TCAGGTCTCAGCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGATGCC	1080
1081	ATGCCCCCGGAGCTGAGGCTTTATGAGCTCCAGGGTACCAGCAAGCATGACTCATCC	1140
1081	ATGCCCCCGGAGCTGAGGCTTTATGAGCTCCAGGGTACCAGCAAGCATGACTCATCC	1140
1141	TTCCAGGGCACCAGACAGACTCTGCGGGGACCCCTTGTCTCCAGGTGACTGCTAA	1197
1141	TTCCAGGGCACCAGACAGACTCTGCGGGGACCCCTTGTCTCCAGGTGACTGCTAA	1197
RESULT 3		
DQ045549	Pan troglodytes FLJ34633 gene, VIRUTAL TRANSCRIPT, partial sequence, genomic survey sequence.	
LOCUS	DQ045549.1 GI:66896764	
DEFINITION	Pan troglodytes (chimpanzee)	
ACCESSION	DQ045549	
VERSION	DQ045549.1	
KEYWORDS	GSS.	
SOURCE	Pan troglodytes	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.	
REFERENCE	1 (bases 1 to 1181)	
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.	
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees	
JOURNAL	(er) PLoS Biol. 3 (6), E170 (2005)	
PUBMED	15869325	
REFERENCE	2 (bases 1 to 1181)	
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.	
TITLE	Direct Submission	
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.	
FEATURES	Location/Qualifiers	
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gene	/organism="Homo sapiens"	
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	/gene="FLJ34633"	
	/locus_tag="HC11301"	
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Best Local Similarity	100.0%; Pred. No. 1.1e-296; Mismatches 0; Gaps 0;	
Matches 1197; Conservative	0; Indels 0;	
Qy	1 ATCCCCCGCTGGACACCCCGCCAGCATCTGGGCTTCCACGCTTGGACCGTGGGAG	60
Db	1 ATCCCCCGCTGGACACACCCCGCCAGCATCTGGGCTTCCACGCTTGGACCGTGGGAG	60
Qy	61 CGGCCAACAGAGTATGCTGGAGACATATGATAAACCACTCAGCCGCCACCAAGCGCG	120
Db	61 CGGCCAACAGAGTATGCTGGAGACATATGATAAACCACTCAGCCGCCACCAAGCGCG	120
Qy	121 CGCACCCCTAGACACACCCCAAGGACCTCGGCCACCATGGGCCAGAGACATACCTTC	180
Db	121 CGCACCCCTAGACACACCCCAAGGACCTCGGCCACCATGGGCCAGAGACATACCTTC	180
Qy	181 ATCTCTGGCTCTGCTGAGCGGCGCTTGAAGTCCCGACCTGCTGCTCTGCGGACCC	240
Db	181 ATCTCTGGCTCTGCTGAGCGGCGCTTGAAGTCCCGACCTGCTGCTCTGCGGACCC	240
Qy	241 TGGGTGAGAGTGCTGCGGGCTGCTTCTGCTTCCGCGGCTGCGGGATGCTCTCAG	300
Db	241 TGGGTGAGAGTGCTGCGGGCTGCTTCTGCTTCCGCGGCTGCGGGATGCTCTCAG	300
Qy	301 CGCTGAGGAGCTGCTGCGGGGATGACGACCCCTGCTCTACTGAGGACTCCACTGAG	360
Db	301 CGCTGAGGAGCTGCTGCGGGGATGACGACCCCTGCTCTACTGAGGACTCCACTGAG	360
Qy	361 GGGACTGCTGAAGCCAACTGGGCGGAGACCAATGGAGTGCCCCCGGCGCTGCTCGT	420
Db	361 GGGACTGCTGAAGCCAACTGGGCGGAGACCAATGGAGTGCCCCCGGCGCTGCTCGT	420
Qy	421 GCACCCCGGAGCGGGGATGGCGAGGCTCAAGTCAACCATGGGAGGAGCTTCAGC	480
Db	421 GCACCCCGGAGCGGGGATGGCGAGGCTCAAGTCAACCATGGGAGGAGCTTCAGC	480
Qy	481 TACCCCGATTTAAGCTCAAGGACATCCTGTGTATCCCTACCGAGGGCCACCTCCCA	540
Db	481 TACCCCGATTTAAGCTCAAGGACATCCTGTGTATCCCTACCGAGGGCCACCTCCCA	540
Qy	541 GCCCTGATGCGGACTCTGCTGCAAGGAGCAGCTGGCGGATCCCGACCATCGCAC	600
Db	541 GCCCTGATGCGGACTCTGCTGCAAGGAGCAGCTGGCGGATCCCGACCATCGCAC	600
Qy	601 AGCTGCCCGACACCTTTGCCAGTAGTCTCTGTGGCTCCGAGGAGTACTATTCTTTCCAT	660

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		Query Match 66.8%; Score 1145; DB 11; Length 1181; Best Local Similarity 97.2%; Pred. No. 2.6e-283; Matches 1148; Conservative 0; Mismatches 33; Indels 0; Gaps 0;			
ORIGIN					
QY	1	ATGCCCGCCCTGGACACCCCGCCAGCATCTGGGCTCCAGCTTGGAGCCGTGGGAG	60		
Db	1	ATGCCCGCCCTGGACACCCCGCCAGCATCTGGGCTCCAGCTTGGAGCCGTGGGAG	60		
QY	61	CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACTCAGCCCCCAACAGCCGC	120		
Db	61	CGGCCAACAGAGCTATGTCTGGNNAATATGATAAACCACTCAGCCCCCAACAGCCGC	120		
QY	121	CGACCCGTAGACACACCCAGGACCTTGGCCACCATGGGCCAGAGCAATTACCTTC	180		
Db	121	CGACCCGTAGACACACCCAGGACCTTGGCCACCATGGGCCAGAGCAATTACCTTC	180		
QY	181	ATCTCTGGCTCTGCTGAGCGGGCCCTTGAGTTCCTCCACCTGCTGCTCTGGCGACCC	240		
Db	181	ATCTCTGGCTCTGCTGAGCGGGCCCTTGAGTTCCTCCACCTGCTGCTCTGGCGACCC	240		
QY	241	TGGGTGTGGAGTGTGTCGGGCTGCTTCTGCTTCGGCGCTGCGGGATGTCCTCCAG	300		
Db	241	TGGGTGTGGAGTGTGNNNCGGNNCTTNNGCTTCGGCGCTGCGGGATGNNCTCCAG	300		
QY	301	CGCTGTGGAGCTGTGTGGGGATGACGCCCTGCTGTCTACTAGGAGTCCACTGAG	360		
Db	301	CGCTGTGGNNCTGTGTGGGGATGACGCCCTGCTGTCTACTAGGAGTCCACTGAG	360		
QY	361	GGGACTGCTGAAGCCAACTGGGCCAAGGAGCAATGAGTGTGCCCCCAGCCCTGATCGT	420		
Db	361	GGGACTGCCGAAGCCAACTGGGCCANGGAGCAATGAGTGTGCCCCCAGCCCTGATCGT	420		
QY	421	GCACCCCGCAGCGCGGGATGGCAGCGGCTCAAGTCAACCATGGGAGCAGCTTCAGC	480		
Db	421	GCACCCCGCAGCGCGGGATGGCAGCGGCTCAAGTCAACCATGGGAGCAGCTTCAGC	480		
QY	481	TACCCCGATGTTAAGCTCAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACTCCCA	540		
Db	481	TACCCCGATGTTAAGNTCAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACTCCCA	540		
QY	541	GCCCTGTATGCGGACTCCTGCTGCAAGGAGCCACTGGCCGATCCCCCAGCCATCGACAC	600		
Db	541	GCCCTGTATGCGGACTCCTGCTGCAAGGAGCCACTGGCCGATCCCCCAGCCATCGACAC	600		
QY	601	AGCTGCCAGCAGCACTTTGCCAGTAGTCTCTGTGGCTCCGAGGAGTACTATTCTTTCCAT	660		
Db	601	AGCTGCCAGCAGCACTTTGCCAGTAGTCTCTGTCCTGTTNAGGAGTACTATTCTTTCCAT	660		
QY	661	GAGTCGAGCTGGACCTGCCGAGATGGCAGTGGCTCCATGTCGAGCCGAGAAATTGAT	720		
Db	661	GAGTCGAGCTGGACCTGCCGAGATGGCAGTGGCTCCATGTCGAGCCGAGAAATTGAT	720		
QY	721	GTGCTCATCTTCAAGAGCTGACAGAGCTGTTCCAGCGTACACAGATCGATGAGCTGGCC	780		
Db	721	GTGCTCATCTTCAAGAGCTGACAGAGCTGTTCCAGCGTACACAGATCGATGAGCTGGCC	780		
QY	781	AAGTGCAATCAGACACTGTGTTCTCGAGAAGACCAAGTAAAGTCTCGGACCTTATCAGC	840		
Db	781	AAGTGCAATCAGACACTGTGTTCTCGAGAAGACCAAGTAAAGTCTCGGACCTTATCAGC	840		
QY	841	AGCATCAGCAGGACTACCACTCGATGAGCAGGATGCTGAGGGCCGCTGTGACCGGC	900		
Db	841	AGCATCAGCAGGACTACCACTCGATGAGCAGGATGCTGAGGGCCGCTGTGACCGGC	900		
QY	901	ATCATTTGCAATTAGTACCCGAAAGACCGGTGCTCGCCCCACAGACCTCGGAGGGTCTGTTCA	960		
Db	901	ATCATTTGCAATTAGTACCCGAAAGACCGGTGCTCGCCCCACAGACCTCGGAGGGTCTGTTCA	960		

Db	901	ATCATTTGCAATTAGTACCCGAAAGACCGGTGCTCGCCCCACAGACCTCGGAGGGTCTGTTCA	960		
QY	961	ACTCGGGCTGTGCCCCAACACCGCTGCTGCCCCCTGACAGTGGCCATGAGACCATGGTGGCC	1020		
Db	961	ACTCGGGCTGTGCCCCAACACCGCTGCTGCCCCCTGACAGTGGCCATGAGACCATGGTGGCC	1020		
QY	1021	TCAGGTCTTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCGAGGAGACGACTGCAGATGCC	1080		
Db	1021	TCAGGTCTTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCGAGGAGACGACTGCAGATGCC	1080		
QY	1081	ATCGCCCCGAAGCTGAGGCGCTTATGAGAGCTCCACGGGTACCCAGCAAGCCATGACTCATCC	1140		
Db	1081	ATCGCCCCGAAGCTGAGGCGCTTATGAGAGTCCAGGGTACCCAGCAAGCCATGACTCATCC	1140		
QY	1141	TTCCAGGGSCACCGACACAGACTCTCTGCGGGGSCACCTTGTCT	1181		
Db	1141	TTCCAGGGSCACCGACACAGACTCTCTGCGGGGSCACCTTGTCT	1181		
RESULT 4					
AK007551					
LOCUS					
DEFINITION					
Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810019J16 product:SIMILAR TO PATA BOX BINDING PROTEIN (TBP)-ASSOCIATED FACTOR, RNA POLYMERASE II, CL, 130KD homolog [Mus musculus], full insert sequence.					
AK007551					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
Mus musculus					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
1					
Carninci, P. and Hayashizaki, Y.					
High-efficiency full-length cDNA cloning					
Meth. Enzymol. 303, 19-44 (1999)					
10349636					
2					
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.					
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes					
Genome Res. 10 (10), 1617-1630 (2000)					
11042159					
3					
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Harada, A., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.					
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer					
Genome Res. 10 (11), 1757-1771 (2000)					
11076861					
4					
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.					
Functional annotation of a full-length mouse cDNA collection					
Nature 409, 685-690 (2001)					
5					
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.					
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs					
Nature 420, 563-573 (2002)					
6 (bases 1 to 1657)					
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,					

901	ATCATTTGCATTAGTACCCGAAAGACGCGTCTCGCCCCACAGACCTCGGAGGGTCTGTTCA	960
961	ACTCGGGCTGCTGCCCAAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGC	1020
961	ACTCGGGCTGCTGCCCAAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGC	1020
1021	TCAGGTCTCAGCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGATGCC	1080
1021	TCAGGTCTCAGCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGATGCC	1080
1081	ATGCCCCGAACTGAGGCTTATGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC	1140
1081	ATGCCCCGAACTGAGGCTTATGAGTTCAGGGTACCCAGCAGCAGTACTCATCC	1140
1141	TTCCAGGGCACCAGACACAGACTCTCGGGGGCACCTTGCT	1181
1141	TTCCAGGGCACCAGACACAGACTCTCGGGGGCACCTTGCT	1181

RESULT 4

AK007551

LOCUS

DEFINITION

Mus musculus 1657 bp mRNA linear HTC 03-APR-2004

enriched library, clone:1810019J16 product:SIMILAR TO TATA BOX

BINDING PROTEIN (TBP)-ASSOCIATED FACTOR, RNA POLYMERASE II, C1,

130KD homolog [Mus musculus], full insert sequence.

ACCESSION

AK007551.1 GI:12841167

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1

REFERENCE

AUTHORS

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

10349636

2

REFERENCE

AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

11042159

3

REFERENCE

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

11076861

4

REFERENCE

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

REFERENCE

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 1657)

REFERENCE

AUTHORS

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,


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QY 1200 CTTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGCCCTACAGAAATGAAGAGG 1259
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QY 1260 GGGACAGGAACCC---CTGTGGGAGAGGCTTAGACCTGAAGCAGTGGCCACTCTGGCTC 1316
|||
Db 1300 GGAACAGGACCTCTGTGTGGGCGCCCTCTGAGCCACAGAGCAGTGAACCTCTCTGGCTT 1359
|||
QY 1317 CTCTGCTTGGCTGAGTGGTCTCTGGACCATGTGCATTTCTAGGGCCATGGATCTTA 1376
|||
Db 1360 TTGCTTTTGTGAATCC-----CTTAGACCAATATATTTACAGGGGCATGGTCCCA 1414
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QY 1377 CATTCTCTTGCATCCCGAGCTGTCTGATCCCTGCCAGGCGCCCTTC 1423
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RESULT 5
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AGENCOURT_6420313 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502726
5', mRNA sequence.
BM460277
BM460277.1 GI:18509317
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 975)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
TITLE
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12141 row: F column: 07
High quality sequence stop: 659.
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/notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 46.9%; Score 803.6; DB 3; Length 975;
Best Local Similarity 98.5%; Pred. No. 2e-195;
Matches 832; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

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Db 1 CCCAGCACCTTTGCCAGTAGTCTCTGGCTCCGAGGAGTACTATTCTTTCCATGAGTCG 60
|||
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QY 787 ACATCAGACACTGTGTTCTGTGAGAGAACCAAGTAAGATCTCGGACCTTATACGACGATC 846
|||
Db 181 ACATCAGACACTGTGTTCTGTGAGAGAACCAAGTAAGATCTCGGACCTTATACGACGATC 240
|||
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|||
Db 301 CGCATTAGTACCCGAAAGAGCCGCTGCTGCCCCACAGACCTCGGAGGGTGTTCACATCGG 360
|||
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|||
Db 361 GCTGTGCCCCAAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGATGGTGGCTCAGT 420
|||
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|||
Db 421 CTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGAGACACTGCAGATGCCATCGCC 480
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QY 1087 CGGAAGCTGAGGCTTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCTTCCAG 1146
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Db 481 CGGAAGCTGAGGCTTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCTTCCAG 540
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QY 1267 GGAACCCCTGTGGGAGAGGCTTAGACCTGAACAGCAGTGCCCACTCTGGCTCTCTGCCCT 1326
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QY 1444 GGTGG 1448
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Db 841 AGGGG 845
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RESULT 6
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LOCUS AK051860.1 GI:26342255
DEFINITION Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length
enriched library, Clone:D23001M17 product:hypothetical protein,
full insert sequence.
ACCESSION AK051860
VERSION AK051860.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
AUTHORS High-efficiency full-length cDNA cloning
TITLE Meth. Enzymol. 303, 19-44 (1999)
JOURNAL 10349636
PUBMED
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
```

Itou, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
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prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159

REFERENCE
AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
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11076861

TITLE
JOURNAL
PUBLISHED
REFERENCE
AUTHORS

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PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

TITLE
JOURNAL
PUBLISHED
REFERENCE
AUTHORS

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Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1596)

TITLE
JOURNAL
PUBLISHED
REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission

TITLE
JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES
source

1. 1596
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:D230011M17"
/db_xref="taxon:10090"
/clone="D230011M17"
/tissue_type="eyeball"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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890. 1432
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(evidence: decoder, Longest-ORF)
putative"
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CDS

ORIGIN
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Matches 891; Conservative 0; Mismatches 145; Indels 3; Gaps 1;
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DB 1353 ATGCCAGGCGGGACAGCCCGCCCATCATCTGGGCTCCAGCTTGGGCGCCCTGGAG 1294
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DB 1293 AGCCCATCAGAGTTATGCTGGGAAACGACGATGAGGCTCCAGCCGCCACCGGCGCT 1234
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DB 1233 CGCACCCAGGAGGCGACACCTTAAGGACCTTGGCCACCATGGGCGAGAGTATCACCTTC 1174
QY 181 ATCTCTGGCTCTGCTGAGCGGCGCTTGTAGTCCCCCACCCTGCTGCTCTGGCGACCC 240
DB 1173 ATTTAGGCTCTGACAGAACGACCAAGAGCCCCCACTGCTGCTCTCTGGCGCCCC 1114
QY 241 TGGGTGTGGAGTGGTGGCGGCGCTTCTGTCTCCGCGCTGCGGGGATGCTCTCCAG 300
DB 1113 TGGGGTTGGAGTGGTGGAGGCTGCTTCTGTCTCGAGCGCTGAGGAGTTCCTTCGAG 1054
QY 301 CGCTGTGGAGCTGTGTGGGGGATCGACCCCTGCTGCTGTCTACTGAGGATCTCACTGAG 360
DB 1053 CGCTGTGGGCTTGTGTGGCGGCTGTCAGCCCTGCTGTCTGCTCCGAGAGACCCCATTTGAA 994
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DB 993 GGGTCTGCCGAAGCCCTTGGGCGAAGGAGCAACAATGGTGTGCCCCCAGCCAGACCGT 934
QY 421 GCACCCCGGAGCGGGGATGGCGAGCGCTCAAGTCAACCATGGGAGCAGCTTCAGC 480
DB 933 GCACCCCGGAGCGCGGATGGCGAGCGCTCAAGAGCATGGGAGCAGCTTCAGC 874
QY 481 TACCCCGATGTTAAGCTCAAGGATCCCTGTGTGTATCCCTACCCGAGGCGCACCTCCCCA 540
DB 873 TACCTGTATGTTAAGCTCAAGGATCCCTGTGTATCCCTACCCGATGCGCACCTCCCCA 814
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DB 813 GTCCCTGAGCTGGAGCTCTGCTGCAAGGAGCCCTGGCGGAGCTCTCCCGAGCGGAC 754
QY 601 AGCTGCCCGAGCAGCTTTGCGAGTAGTCTCTGGGCTCGAGGAGTACTATTCTTTCCAT 660
DB 753 AGCTGCCCTAGCACCTTACCAACGCCCGCGGCTCTGAGGAGTACTACTCTTTCAT 694
QY 661 GAGTGGAGCTGGAGCTTGGCGAGATGGGAGTGGCTTCCATGTCGAGCCGAGAAATGAT 720
DB 693 GAATCGGACTGGACCTGCTGAGATGGGAGTGGCTTCCATGTCGAGCGGGAGATCGAC 634
QY 721 GTGCTCATCTTCAAGAGCTGACAGAGCTGTTTCAGGCTGACACAGATCGATGAGCTGGCC 780
DB 633 GTGCTTATTTTCAAGAGCTGACAGAGCTGTTTCAGGCTGACACAGATGACGAGCTGGCC 574
QY 781 AAGTGACATCAGACACTGTGTTCTCGGAGAGAGCAGTAAGATCTCGGACCTTTATCAGC 840
DB 573 AAGTGACATCAGACACTGTGTTCTCGGAGAGAGCAGTAAGATCTCGGACCTTTATCAGC 514
QY 841 AGCATCAGCAGGACTTACCACTTGGATGAGCAGGATGCTGAGGCGCGCTTGTGTCGCGG 900
DB 513 AGCATCAGCAGGACTTACCACTTGGATGAGCAGGATGCTGAGGCGCGCTTGTGTCGCGG 454
QY 901 ATCATTTGCATTTAGTACCCGAAAGAGCCGCTGCTGCGCCCAAGACCTCGGAGGGTCTGTTCA 960

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Db 453 ATCATCGATTATTACCCGCAAAAGCGCTCCCGCCACAGACCTCCCGAGGGGCGCTCA 394
QY 961 ACTCGGGCTGTCGCCCAACCGCTGTGCCCTTGACAGTGGCCATGAGACCATGTGTGGGC 1020
Db 393 GCCCGCTCTACTGCC--CTGCTGTGCCCGCCGACAGTGGCCATGAGACCATGTGTGGGC 337
QY 1021 TCAGGTCTCAGCCAGGATG 1039
Db 336 TCGGCTCAGCCAGGACG 318

RESULT 7
CN289134
LOCUS 170059993535 GRN_PREHEP Homo sapiens cDNA 5', mRNA linear EST 16-MAY-2004
DEFINITION CN289134
ACCESSION CN289134
VERSION CN289134.1 GI:47305548
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 753)
AUTHORS Brandenberger R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M. S., Mandalam, R.,
Lebkowski, J. and Stanton, L. W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 753 Std Error: 0.00.
Location/Qualifiers
1..753
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/db_xref="taxon:9606"
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line"
/clone_lib="GRN PREHEP"
/note="Oligo dT primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

FEATURES
source
Query Match 42.7%; Score 731.4; DB 7; Length 753;
Best Local Similarity 99.7%; Pred. No. 7.4e-177;
Matches 743; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

ORIGIN
QY 267 CTTCTGCTTCGCGCGTGC CGGGATTGCTCTCAGCGCTGTGAGCCTGTGTGCGGGGATG 326
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QY 327 CAGCCCCCTGCTCTACTGAGGACCTCCACTGAGGGGACTGCTGAAGCCAACTGGGCCAA 386
Db 69 CAGCCCCCTGCTCTACTGAGGACCTCCACTGAGGGGACTGCTGAAGCCAACTGGGCCAA 128
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Db 129 GGAGCACAATGGAGTGC CCCCCCAGCTGCTGATGTCACCCCCCAGCCCGCGGGATGGCC 188
QY 446 AGCGGCTCAAGTCAACCATGGGAGCAGCTTACGCTACCCCGATGTTAAGCTCAAAGGCA 505
Db 189 AGCGGCTCAAGTCAACCATGGGAGCAGCTTACGCTACCCCGATGTTAAGCTCAAAGGCA 248
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QY 566 AGGAGCCACTGTGCCCATGCCCAACCATGCGACACAGCTGCCAGCACTTTGCCAGTA 625
Db 309 AGGAGCCACTGTGCCCATGCCCAACCATGCGACACAGCTGCCAGCACTTTGCCAGTA 368
QY 626 GTCCCTGTGGCTCCGAGGAGTACTATTCTTCCATGAGTGGAGCTGGACCTGCCGAGA 685
Db 369 GTCCCTGTGGCTCCGAGGAGTACTATTCTTCCATGAGTGGAGCTGGACCTGCCGAGA 428
QY 686 TGGGAGTGGCTCCATGTGCGAGCCGAGAAATGTGTGTGCTCATCTTCAAGAAGCTGACAG 745
Db 429 TGGGAGTGGCTCCATGTGCGAGCCGAGAAATGTGTGTGCTCATCTTCAAGAAGCTGACAG 488
QY 746 AGCTGTTCAGCGTACACCCAGATCGATGAGCTGGCCAAAGTGCACATAGACACTGTGTTC 805
Db 489 AGCTGTTCAGCGTACACCCAGATCGATGAGCTGGCCAAAGTGCACATAGACACTGTGTTC 548
QY 806 TGGAGAGACCAAGTAAGATCTCGGACCTTATCAGCAGCATCAGCAGGACTACCACTGG 865
Db 549 TGGAGAGACCAAGTAAGATCTCGGACCTTATCAGCAGCATCAGCAGGACTACCACTGG 608
QY 866 ATGAGCAGGATGCTGAGGGCCGCTGGTACGGCGGATCATTCGCATTAGTACCCGAAAGA 925
Db 609 ATGAGCAGGATGCTGAGGGCCGCTGGTACGGCGGATCATTCGCATTAGTACCCGAAAGA 668
QY 926 GCCGTGCTCGCCACAGACCTCGGAGGGTCTTCAACTCGGGCTGTGTCGCCCAACCGCTG 985
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QY 986 CTGCCCTGACAGTGGCCATGAGAC 1010
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RESULT 8
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ACCESSION BO691555
VERSION BO691555.1 GI:21816871
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 917)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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/notes="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 40.1%; Score 687; DB 5; Length 917;
Best Local Similarity 98.3%; Pred. No. 2.1e-165;
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RESULT 9

BY707606

LOCUS

DEFINITION

musculus cDNA clone 181019J16 5', mRNA sequence.
1009 bp mRNA linear EST 16-DEC-2002

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

BY707606 GI:27118783
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 1009)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dregani, T.A.,
Fletcher, C.P., Forrest, A., Fraser, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
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Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
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Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravaei, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verrardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynnshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kitahara, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE
JOURNAL
PUBMED
COMMENT

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12456851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for

Db	824	CAAGTGCACATCGGACACCGGTGCTCCTGGAGAGACACGACAGATCTCAGACCTGATCAG	883
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REFERENCE	1 (bases 1 to 1015)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLC810 row: d column: 06 High quality sequence stop: 752. Location/Qualifiers 1. 1015 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3947861" /tissue_type="adenocarcinoma cell line" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_9" /note="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."		
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Hominidae; Homo.			
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1 (bases 1 to 1015)			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
Contact: Robert Strausberg, Ph.D.			
Email: cgapbs-remail.nih.gov			
Tissue Procurement: DCTD/DTF			
cDNA Library Preparation: Ling Hong/Rubin Laboratory			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Incyte Genomics, Inc.			
Clone distribution: MGC Clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov			
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EcoRI; cDNA made by oligo-dT priming. Directionally			
cloned into EcoRI/XhoI sites using the following 5'			
adaptor: GGCACGAG(G). Size-selected >500bp for average			
insert size 1.8kb. Library constructed by Ling Hong in			
the laboratory of Gerald M. Rubin (University of			
California, Berkeley) using ZAP-cDNA synthesis kit			
(Stratagene) and Superscript II RT (Life Technologies)."			
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Query Match			
Best Local Similarity 39.1%; Score 669.4; DB 2; Length 1015;			
Matches 837; Conservative 0; Mismatches 66; Indels 18; Gaps 11;			
Qy	63	GCGAAGCAGAGCTATGCTCTGGAGACATATGATAAACCACTCTAGCCCCCAGCGCGCG	122
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Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 966)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

Query Match	Best Local Similarity	Score	DB 2;	Length
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			Gaps	7;
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Qy	880	GAGGGCCGCTGGTACCGGCATCATTTCCGATTAGTACCCGAAAGAGCCGTGCTCGCCCA	939		
Db	422	GAGGGCCGCTGGTACCGGCATCATTTCCGATTAGTACCCGAAAGAGCCGTGCTCGCCCA	481		
Qy	940	CAGACCTTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCAACCGCTGCTGCCCTTGACAGT	999		
Db	482	CAGACCTTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCAACCGCTGCTGCCCTTGACAGT	541		
Qy	1000	GGCCATGAGACCAATGTTGGGCTCAGTCTCAGCCAGGATGA	1040		
Db	542	GGCCATGAGACCAATGTTGGGCTCAGTCTCAGCCAGGATGA	582		

RESULT 14	
B1694617	
LOCUS	826 bp mRNA linear EST 18-SEP-2001
DEFINITION	G0334783BF1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5375384 5'; mRNA sequence.
ACCESSION	B1694617
VERSION	B1694617.1 GI:15657246
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 826) NTH-WGC http://wgc.nci.nih.gov/ .
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE	Unpublished (1999)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs-x@mail.nih.gov
COMMENT	Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) cDNA Sequencing bv: Invctv Genomics, Inc.

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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1955 row: 1 column: 09
High quality sequence stop: 796.
      Location/Qualifiers
1. 826
   /organism="Mus musculus"
   /mol_type="mRNA"
   /strain="FVB/N-3"
   /db_xref="taxon:10090"
   /clone="IMAGE:5375384"
   /tissue_type="tumor, biopsy sample"
   /dev_stage="5 months"
   /lab_host="DH108"
   /clone_lib="NCI_CGAP_Mam2"
   /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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ORIGIN

[illegible]

QY 1018 GGCTCAGGTCCTCAGCCA--GGATGAGCTCAGAGTCAGATCTCCACGAGAGCAGACTGCAG 1075
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Db 717 GGCTCTGGGCTCAGCCACGACGAACTGACAGTCCAGATCTCCCGAGGAGCAACCGGA 776
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QY 1076 ATGCCATCGCCGGAGAGCTGAGGCC 1100
|||||
Db 777 GATGCATCGCCAGGAACTGAGGC 801
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RESULT 15

BP331524
LOCUS BP331524 Sugano cDNA library, rectum Homo sapiens cDNA clone
DEFINITION RCT09504, mRNA sequence.

ACCESSION BP331524

VERSION BP331524.1 GI:52260875

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 (bases 1 to 583)

Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="RCT09504"
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ORIGIN

Query Match 31.5%; Score 540.2; DB 3; Length 583;

Best Local Similarity 98.3%; Pred. No. 1.2e-127;

Matches 575; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

QY 19 CCCCCCAGCATCTGGGCTCCACGCTTGGACCGTGGAGCGGCCAACAGAGCTA-TG 77
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Db 1 CCCCCCAGCATCTGGGCTCCACGCTTGGACCGTGGAGCGGCCAACAGAGCTATTG 60
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QY 78 TCTGGAGACATATGATAAACCACTCTCAGCCCCCACCACCGCCGACCCGTAGACCAGA 137
|||||

Db 61 TCTGGAGACATATGATAAACCACTCTCAGCCCCCACCACCGCCGACCCGTAGACCAGA 120
|||||

QY 138 CCCCAGGACCTTGGCCACCATGGGCCAGAGACATTACTTTCATCTCTGGCTCTGCTGA 197
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Db 121 CCCCAGGACCTTGGCCACCATGGGCCAGAGACATTACTTTCATCTCTGGCTCTGCTGA 180
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QY 198 GCGGGCCCTTGAGTCCGCCACCTGCTGCTCTGCGCACCTGGAGTGGAGTGGTG 257
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Db 181 GCGGGCCCTTGAGTCCGCCACCTGCTGCTCTGCGCACCTGGAGTGGAGTGGTG 240
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QY 258 CCGGGCTGCTTCTGCTTCCGCGCTCCGGGATTGCTCCAGCGCTGTGGAGCCTGTGT 317
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Db 241 CCGGGCTGCTTCTGCTTCCGCGCTCCGGGATTGCTCCAGCGCTGTGGAGCCTGTGT 300
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QY 318 GCGGGGATGAGCCCTTGCCTGTCTACTGAGGACTCCACTGAGGGGAGCTGCTGAAGCCAA 377
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Db 301 GCGGGGATGAGCCCTTGCCTGTCTACTGAGGACTCCACTGAGGGGAGCTGCTGAAGCCAA 360
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QY 378 CTGGGCCAAGGAGCACAATGGAGTCCCCCAGCCCTGATCGTGCACCCCCAGCCGGCG 437
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Db 361 CTGGGCCAAGGAGCACAATGGAGTCCCCCAGCCCTGATCGTGCACCCCCAGCCGGCG 420
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QY 438 GGATGGCCAGCGGCTCAAGTCAACCATGGGCGAGCAGCTTCAGCTACCCGATGTTAAGCT 497
|||||
Db 421 GGATGGCCAGCGGCTCAAGTCAACCATGGGCGAGCAGCTTCAGCTACCCGATGTTAAGCT 480
|||||
QY 498 CAAAGGCATCCCTGTGTATCCCTACCGAGGGCCACCTCCCGAGCCCTGTGATGCGGACTC 557
|||||
Db 481 CANAGGCATCCCTGTGTATCCCTACCGAGGGCCACCTCCCGAGCCCTGTGATGCGGACTC 540
|||||
QY 558 CTGCTGCAAGGAGCCACTGGCCGATCCCCACCCATGCGACACAG 602
|||||
Db 541 CTGCTGCAAGGA-CCACTGGCCGAT-CCCCACCCATGCGACACAG 583
|||||

Search completed: March 11, 2006, 22:01:33

Job time : 6313 secs

Result No.	Score	Query Match	Length	DB	ID	Description	
C 1	1692.8	98.8	1785	3	US-10-104-047-799	Sequence 799, App	
C 2	46	2.7	4403765	3	US-09-103-840A-2	Sequence 2, Appl	
C 3	42.2	2.5	1767	3	US-09-016-434-1488	Sequence 1488, Ap	
C 4	41.4	2.4	2109	3	US-09-370-838-153	Sequence 153, App	
C 5	41.4	2.4	2109	3	US-09-854-133-153	Sequence 153, App	
C 6	40.8	2.4	438	3	US-09-489-039A-6029	Sequence 6029, Ap	
C 7	40.8	2.4	465	3	US-09-489-039A-6072	Sequence 6072, Ap	
C 8	40.8	2.4	930	3	US-09-489-039A-6078	Sequence 6078, Ap	
C 9	40.4	2.4	1503	3	US-09-797-039-3	Sequence 3, Appl	
C 10	40.4	2.4	2297	3	US-09-797-039-1	Sequence 1, Appl	
C 11	40.4	2.4	2747	3	US-09-620-312D-19	Sequence 19, Appl	
C 12	40.4	2.4	2840	3	US-09-620-312D-20	Sequence 20, Appl	
C 13	40.4	2.4	3124	3	US-09-734-030-1	Sequence 1, Appl	
C 14	40.4	2.4	3124	3	US-10-153-921-1	Sequence 1, Appl	
C 15	40.4	2.4	3124	3	US-10-669-689-1	Sequence 1, Appl	
C 16	40.2	2.3	975	3	US-09-902-540-9140	Sequence 9140, Ap	
C 17	40.2	2.3	10178	3	US-09-902-540-977	Sequence 977, App	
C 18	40.2	2.3	11935	3	US-09-949-016-14290	Sequence 14290, A	
C 19	40.2	2.3	11935	3	US-09-949-016-14291	Sequence 14291, A	
C 20	39.6	2.3	284	2	US-08-902-623-42	Sequence 42, Appl	
C 21	39.6	2.3	364	3	US-09-621-976-17202	Sequence 17202, A	
C 22	39.4	2.3	7218	2	US-08-232-463-14	Sequence 14, Appl	
C 23	39.2	2.3	430	3	US-09-621-976-16656	Sequence 16656, A	
C 24	39.2	2.3	1336	3	US-09-902-540-1945	Sequence 1945, Ap	

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Db 450 GGGACTGCTGAAGCCAACTGGGCGAAGGAGCACAATGAGTGTGCCCCCGAGCCCTGATCGT 509
QY 421 GCACCCCCCAGCGCGGGGATGCGCAGCGGCTCAAGTCAACCATGAGGCGAGCTTCAGC 480
Db 510 GCACCCCCCAGCGCGGGGATGCGCAGCAGCTCAAGTCAACCATGAGGCGAGCTTCAGC 569
QY 481 TACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGCGCACTCCCCA 540
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QY 541 GCCCTGTATGCGGACTTCCTGCTCAAGGAGCCACTGCGCGGATCCGCCCAACCATGCGACAC 600
Db 630 GCCCTGTATGCGGACTTCCTGCTCAAGGAGCCACTGCGCGGATCCGCCCAACCATGCGACAC 689
QY 601 AGCCTGCCCAGCACCCTTTGCCAGTAGTCTCTCGTGGCTCCGAGGAGTACTTCTTTCCAT 660
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QY 661 GAGTGGGACTGTGACCTGCGCGGAGATGGGAGTGGCTCCATGTCGAGCGCGAGAAATTGAT 720
Db 750 GAGTGGGACTGTGACCTGCGCGGAGATGGGAGTGGCTCCATGTCGAGCGCGAGAAATTGAT 809
QY 721 GTGCTCATCTTCAAGAAGCTGCAGAGCTGTTTCAGCGTACACAGATCGATGAGCTGGCC 780
Db 810 GTGCTCATCTTCAAGAAGCTGCAGAGCTGTTTCAGCGTACACAGATCGATGAGCTGGCC 869
QY 781 AAGTGACACATCAGACACTGTGTTCTCTGGAGAACACCAAGTAAAGTCTCGGACCTTATCAGC 840
Db 870 AAGTGACACATCAGACACTGTGTTCTCTGGAGAACACCAAGTAAAGTCTCGGACCTTATCAGC 929
QY 841 AGCATCAGCGAGACTACCACTCTGATGATGAGAGGATGCTGAGGCGCGCTGTGTAACGCGC 900
Db 930 AGCATCAGCGAGACTACCACTCTGATGATGAGAGGATGCTGAGGCGCGCTGTGTAACGCGC 989
QY 901 ATCATTTCGATAGTACCGGAAGAGCGCTGCTCGCCACAGACCTCGGAGGGTCTGTCA 960
Db 990 ATCATTTCGATAGTACCGGAAGAGCGCTGCTCGCCACAGACCTCGGAGGGTCTGTCA 1049
QY 961 ACTCGGGCTGCTGCCCCAACCGCTGTGCCCCCTGACAGTGGCCATGAGACCATGTTGGGC 1020
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QY 1081 ATGCCCCGAGAGCTGAGGCTTATGAGCTCCAGGGTACCCAGACGCTGATCTATCC 1140
Db 1170 ATGCCCCGAGAGCTGAGGCTTATGAGCTCCAGGGTACCCAGACGCTGATCTATCC 1229
QY 1141 TTCAGGCGACCGACACAGACTCGTCGGGGGACCCCTGTCTCAGAGTGTACTGTCTAACCC 1200
Db 1230 TTCAGGCGACCGACACAGACTCGTCGGGGGACCCCTGTCTCAGAGTGTACTGTCTAACCC 1289
QY 1201 CTGCGAGGCCCCAGCTGCCACACCTTTCTGGGAGAGCATGGCCCTACAGAAAGAGGG 1260
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QY 1261 GGNACAGGAACCCCTGTGGGAGAGGCTTAGACCTGGAAGCTGCGCCACTCTGCTCCTCC 1320
Db 1350 GGNACAGGAACCCCTGTGGGAGAGGCTTAGACCTGGAAGCTGCGCCACTCTGCTCCTCC 1409
QY 1321 TGCCTTTGGTGTACTGTGGTCTCTGGAACCATGTGATTTCACTGGGCGCATGGGATCTACATC 1380
Db 1410 TGCCTTTGGTGTACTGTGGTCTCTGGAACCATGTGATTTCACTGGGCGCATGGGATCTACATC 1469
QY 1381 TCCTTGCATCCCGAGCTGTGCTGATCCCTGCGGAGGCGCCCTTCTCTGCTCATGGTCT 1440
Db 1470 TCCTTGCATCCCGAGCTGTGCTGATCCCTGCGGAGGCGCCCTTCTCTGCTCATGGTCT 1529
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QY 1441 TCAGTGGCGCTGATCATGGAAGTAAAGGAGTTAGGCATTACCTTCTGGAGTGAAACCCCTG 1500
Db 1530 TCAGTGGCGCTGATCATGGAAGTAAAGGAGTTAGGCATTACCTTCTGGAGTGAAACCCCTG 1589
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QY 1561 TCAACAGTTTAAAGAGCTTATCTTAAATGTATTTGTTGGGGGTGGCGAGGGGCCACT 1620
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QY 1621 CTATGTTATGTTAAAGGAGTTGTTCTTGGTCTTGGCTGATGTTCTGTATCTTAAACATGAC 1680
Db 1710 CTATGTTATGTTAAAGGAGTTGTTCTTGGTCTTGGCTGATGTTCTGTATCTTAAACATGAC 1769
QY 1681 CACAGTTTCTAAAGTAC 1696
Db 1770 CACAGTTTCTAAAGTAC 1785

RESULT 2
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: TUBERCULOSIS
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 2.7%; Score 46; DB 3; Length 4403765;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 115; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 108 CCCACCAAGCGCGCAGCCCGTAGACCAGACCCCAAGGACCCCTGGCCACCATGGGCCAGA 167
Db 3929345 CCGCGCCCGCCGCTTCGCGCCGCTCCCAACGCTTCCGCGCGCGCCGCCGCCGCC 3929286
QY 168 GAGCATTACCTTCATCTCTGGCTCTGCTGAGCGCGCCCTTGAGTCCCCACCTGCTGCCT 227
Db 3929285 TCGCTCGCCACGCGCTGTCTTCCGTTCTGCGCGTACACCGGCCCGCGCGTGCCTCG 3929226
QY 228 GCTCTCGCGACCCCTGGGTGTGGGAGTGTGTCGCGGGTGTGCTTCTGCTCCGCGCTGCCG 287
Db 3929225 GTGCCCGCGCGCCCGTTGATGCGCGCGCGCGCGCTTCCGCGCGCGCCCGCTTGGCG 3929166
QY 288 GGAATTGCTTCAGAGCTGTGAGACCTGTGTGCGGGGATGAGAGCCCTTGCC 337
Db 3929165 CTTTGGCCCGCGCGAAGCGCTTTCGCTTCTTGGGAGAGGCGCGCGCTGTC 3929116

RESULT 3
US-09-016-434-1488
; Sequence 1488, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
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APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1488:
SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G995934
US-09-016-434-1488

Query Match 2.5%; Score 42.2; DB 3; Length 1767;
Best Local Similarity 48.3%; Pred. No. 0.42;
Matches 215; Conservative 0; Mismatches 218; Indels 12; Gaps 3;
Qy 2 TGCCCGCCCTGGACACCCCGCCGACATCTGGGCTCCACGCTTGGGACGTGGGAGC 61
Db 199 TGACACGCTGTGGCCCGCCCTTCCCGCTGTGGGCTGGGACTCCCGGG---GGGTGGG 255
Qy 62 GGCCAAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCAGCGGCC 121
Db 256 GGCTCATGAACTCTTCCCGCCACCTCAGGGTCAGCCAGAACCCCTCGAGGTGGG 315
Qy 122 GCACCGGTAGACAGACCCCAAGAGCCCTGGCCACCATGGGCGAGAGACATTACTTCA 181
Db 316 GCTGAGCTCCAGTCCCGCTTCTTGGCTCCAGGGCTGCGCCAGAGTCCATTCCAGGCC 375
Qy 182 TCTCTGGCTGTGAGCGCGCCCTTGAGTCCCGCCACCTGCTGCTGCTCTGGGACCT 241
Db 376 GCAGCGCGCGCCCGCCACCGCCCGCCAGCGCCCGCGCGCGAGCCCTCCAGGTGGACTTG 435
Qy 242 GGGTGTGGAGTGGTGGCGGGCTGCTTCTGCTTCCGCGCGCTGCGCGGATTGCTCCAGC 301
Db 436 CTCCCGGTGTCCCGCGCGCCAGAGTCCCGCGGGCTGCTGGCGCGCTGCGCGGCT 495
Qy 302 GCTGTGAGCTGTGTGCGGGATGACAGCCCTGCTGCTG---TCTACTGAGGACTC--- 353
Db 496 GCTGCGCGCGCTGCTGCGCGCGCCCGCGCCCTGCTGCGCGCGCTCTACGGTGGACACAGCG 555
Qy 354 -CACTGAGGGAGTGTGTAAGCCAACTGGGCGAGGAGCAATGAGTGGCCCCCGCCAGCC 412

Db 556 GCCTGNAAGCAGCCTCGGCGCCCTCCGCCACCCCGCCAGTGTGCGCGCCCGCGGCC 615
Qy 413 CTGATGTGTACACCCCGCAGCGCGC 437
Db 616 GAGCGCGCGCCCGCCCGCTCCGCGC 640

RESULT 4

US-09-370-838-153/c
; Sequence 153, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 153
; LENGTH: 2109
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-370-838-153

Query Match 2.4%; Score 41.4; DB 3; Length 2109;
Best Local Similarity 46.9%; Pred. No. 0.74;
Matches 129; Conservative 0; Mismatches 146; Indels 0; Gaps 0;
Qy 179 TCATCTCTGGCTCTGTGAGCGCGCCCTTGAGTCCCGCCACCTGTGCTGCTCTGGCGAC 238
Db 764 TCTCCCGCGCCCTGCTGTCTGGGGCCCGGGCTTCCCTCGGGGGCCACTTCGCGCTG 705
Qy 239 CTTGGGTGTGGAGTGTGCGGGCTGCTTCTGCTTCCCGCGCTGCGGGATTGCTCC 298
Db 704 GCTCTCGGGGGCGCTGGCTCCAGCCTCTCGGCTGTGCTCCGCTGGCGGTGGCAGCGGT 645
Qy 299 AGCGCTGTGAGCCTGTGTGCGGGGATGACGCCCTGCTGCTACTAGAGACTCCACTG 358
Db 644 GCGCGCGGTGGCTGCGCGCCCTGCTGTGTCTACCCATCGGCCCTTGGCTCCAGCGCCTT 585
Qy 359 AGGGGACTCTGAAGCAACTGGGCGCAAGAGCAATGAGTGGCCCCCGCCAGCCCTGATC 418
Db 584 CCGGGCGCGCCCGCGGGGCGCTCCCGCTGCGCCACTGGGGCTCGGGCCCCCACCACCCGAGG 525
Qy 419 GTGCACCCCGCCAGCGCGGGATGGCAGCGGCTC 453
Db 524 TCCAGCTCCAGCCCTGGGGCTCTGGGCGCCCC 490

RESULT 5

US-09-854-133-153/c
; Sequence 153, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0

Db 332 CGCGCTCGGCTCGATGCTCTGACGGTGCACAGCGCCGCGGACCGTCACTACCTATC 391
Qy 66 AACAGAGCTATGTCTGAGACATATGATAAACCACCTTCAGCCCCCACCAGCGCGCCAC 125
Db 392 TGGCGCGCCGGATCTCGGGGGCAGCTCGCCGACGAGATCGCGCCGACCTCGCGCCA 451
Qy 126 CCGTAGACAGACCCCAAGACCCCTGGCCACCATATGGGCCAGAGACATTAACCTTCATCTC 185
Db 452 GCGCGCTCGCCCGCGGACCTGTCTGTGTGATCGCGCAGCGGCTCTCTTCTCGGCGG 511
Qy 186 TGCTCTGCTGAGCGCGCCCTTCAGTCCCCACCTGCTGCTGCTGCGGACCCCTGGGT 245
Db 512 TAGAGCGCCAGGGGTGCCGTGA-TCCGGCCCTGCTGCCCTATCTGCAGAGCTGGGT 570
Qy 246 GTGGGAGTGTGCGGGCTGCCCTTCTGCTTCGCGCGCTGCGGGATG 293
Db 571 ATCGGCTGCGCGCGGTGGTGGTGGCGCATCAGTCGCGGGTGGCGTG 618

RESULT 9

US-09-797-039-3
; Sequence 3, Application US/09797039
; Patent No. 6730491
; GENERAL INFORMATION:
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
; TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
; FILE REFERENCE: 10448-017001
; CURRENT APPLICATION NUMBER: US/09/797,039
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-797-039-3

Query Match 2.4%; Score 40.4; DB 3; Length 1503;
Best Local Similarity 53.9%; Pred. No. 1.2;
Matches 83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
Qy 713 AAATTGATGTGCTCATCTTCAAGAGCTGCACAGCTGTTTCAGGTACACCATCGATG 772
Db 203 AGAACGAGATAGGCATCTCAAGATGGTGAAGCATCCCAACATCTCTACAGCTGGTGATG 262
Qy 773 AGCTGGCCAAAGTGACATCAGACACTGTGTTCTCTGGAGAGACAGTAAGATCTCGGACC 832
Db 263 TGTGTTGACCCGACGAGGACTTATCTTCTCTGGAGCTGGCCACGGGAGGAGTGT 322
Qy 833 TTATCAGCAGCATCAGCAGGACTTACCATCTGGA 866
Db 323 TTGACTGGATCTGGACGAGGCTACTACTACCGGA 356

RESULT 10

US-09-797-039-1
; Sequence 1, Application US/09797039
; Patent No. 6730491
; GENERAL INFORMATION:
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
; TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
; FILE REFERENCE: 10448-017001
; CURRENT APPLICATION NUMBER: US/09/797,039
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2297
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1656)
; NAME/KEY: misc feature
; LOCATION: (1)...(2297)
; OTHER INFORMATION: n = A,T,C or G
US-09-797-039-1

Query Match 2.4%; Score 40.4; DB 3; Length 2297;
Best Local Similarity 53.9%; Pred. No. 1.4;
Matches 83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
Qy 713 AAATTGATGTGCTCATCTTCAAGAGCTGCACAGCTGTTTCAGGTACACCATCGATG 772
Db 356 AGAACGAGATAGGCATCTCAAGATGGTGAAGCATCCCAACATCTCTACAGCTGGTGATG 415
Qy 773 AGCTGGCCAAAGTGACATCAGACACTGTGTTCTCTGGAGAGACAGTAAGATCTCGGACC 832
Db 416 TGTGTTGACCCGCAAGGAGTACTTTATCTTCTCTGGAGCTGGCCACGGGAGGAGTGT 475
Qy 833 TTATCAGCAGCATCAGCAGGACTTACCATCTGGA 866
Db 476 TTGACTGGATCTCTGGACGAGGCTACTACTACCGGA 509

RESULT 11

US-09-620-312D-19
; Sequence 19, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 658962el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 19
; LENGTH: 2747
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (206)..(1618)
US-09-620-312D-19

	Matches	83;	Conservative	0;	Mismatches	71;	Indels	0;	Gaps	0;
Qy	713	AAATTGATGTCTCATCTTCAAGAAAGCTGACAGAGCTGTTCAGCGTACACACAGATCGATG	772							
Db	413	AGAACGAGATAGGCATCTCAAGATGGTGAAGCATCCCAACATCCTACAGCTGGTGGATG	472							
Qy	773	AGCTGGCCAAAGTGCACATCAGACACTGTGTCCTGGAGAGACCAAGTAAGATCTCGACC	832							
Db	473	TGTTTGTGACCCGCAAGAGTACTTTATCTCTGTGGAGCTGGCCACGGGAGGGAGGTGT	532							
Qy	833	TTATCAGCAGCATCACGACGAGCTACCACTCTGGA	866							
Db	533	TTGACTGGATCCTGGACACAGGGCTACTACTCGGA	566							

RESULT 15
US-10-669-689-1
; Sequence 1, Application US/10669689
; Patent No. 6800471
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000612DIVII
; CURRENT APPLICATION NUMBER: US/10/669,689
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 09/734,030
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/207,281
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3124
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-689-1

Query Match	2.4%	Score 40.4;	DB 3;	Length 3124;
Best Local Similarity	53.9%	Pred. No. 1.6;		
Matches	83;	Conservative	0;	Mismatches 71;
				Indels 0;
				Gaps 0;
Qy	713	AAATTGATGTCTCATCTTCAAGAAAGCTGACAGAGCTGTTCAGCGTACACACAGATCGATG	772	
Db	413	AGAACGAGATAGGCATCTCAAGATGGTGAAGCATCCCAACATCCTACAGCTGGTGGATG	472	
Qy	773	AGCTGGCCAAAGTGCACATCAGACACTGTGTCCTGGAGAGACCAAGTAAGATCTCGACC	832	
Db	473	TGTTTGTGACCCGCAAGAGTACTTTATCTCTGTGGAGCTGGCCACGGGAGGGAGGTGT	532	
Qy	833	TTATCAGCAGCATCACGACGAGCTACCACTCTGGA	866	
Db	533	TTGACTGGATCCTGGACACAGGGCTACTACTCGGA	566	

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Job time : 329 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 20:00:16 ; Search time 1286 Seconds
(without alignments)
11015.120 Million cell updates/sec

Title: US-09-989-890-105
Perfect score: 1713
Sequence: 1 atgccccgcctggacaccc.....tacctggcgcggaccacgc 1713

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.Main:*
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2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1713	100.0	1713	3	US-09-989-890-105 Sequence 105, App
2	1692.8	98.8	1785	6	US-10-104-047-799 Sequence 799, App
3	1602.4	93.5	1977	3	US-09-989-920-56 Sequence 56, Appl
4	1602.4	93.5	1977	3	US-09-989-920-117 Sequence 117, App
5	607.6	35.5	654	5	US-10-074-475-124 Sequence 124, App
6	463.2	27.0	728	9	US-10-779-543-5731 Sequence 5731, App
7	385	22.5	385	3	US-09-989-920-55 Sequence 55, Appl
8	380.2	22.2	386	3	US-09-989-890-104 Sequence 104, App
9	380.2	22.2	386	5	US-10-074-475-123 Sequence 123, App
10	352.6	20.6	393	9	US-10-779-543-10096 Sequence 10096, A
11	347	20.3	427	9	US-10-779-543-12051 Sequence 12051, A
12	300	17.5	300	9	US-10-779-543-1705 Sequence 1705, App
13	298.4	17.4	300	5	US-10-076-555-34 Sequence 34, Appl
14	298.4	17.4	300	9	US-10-779-543-34 Sequence 34, Appl
15	120	7.0	120	3	US-09-989-920-116 Sequence 116, App
16	46.4	2.7	2761	6	US-10-094-749-973 Sequence 973, App
17	45.6	2.7	513	6	US-10-029-386-10967 Sequence 10967, A
18	45.6	2.7	1242	7	US-10-437-963-6792 Sequence 6792, App
19	43	2.5	2359	5	US-10-091-438-44 Sequence 44, Appl
20	43	2.5	2370	3	US-09-764-853-144 Sequence 144, App
21	42.8	2.5	1412	7	US-10-425-114-16503 Sequence 16503, A
22	42.2	2.5	1767	6	US-10-305-720-1488 Sequence 1488, App
23	42.2	2.5	1767	8	US-10-723-860-3497 Sequence 3497, App

24	42.2	2.5	2389	7	US-10-761-169-7	Sequence 7, Appli
25	42.2	2.5	2429	5	US-10-087-192-1181	Sequence 1181, Ap
26	42	2.5	237	6	US-10-029-386-17895	Sequence 17895, A
27	42	2.5	593	6	US-10-029-386-4195	Sequence 4195, Ap
28	42	2.5	1518	9	US-10-450-763-7952	Sequence 7952, Ap
29	42	2.5	1830	9	US-10-450-763-7951	Sequence 7951, Ap
30	41.8	2.4	1696	8	US-10-425-115-120331	Sequence 120331,
31	41.4	2.4	2109	3	US-09-738-973-153	Sequence 153, App
32	41.4	2.4	2109	3	US-09-854-133-153	Sequence 153, App
33	41.4	2.4	2109	5	US-10-144-649A-153	Sequence 153, App
34	41.4	2.4	3267	9	US-10-450-763-28779	Sequence 28779, A
35	41.4	2.4	4988	6	US-10-288-798-48	Sequence 48, Appl
36	41.4	2.4	4988	7	US-10-362-892-48	Sequence 48, Appl
37	41.4	2.4	13862	3	US-09-764-891-5477	Sequence 5477, Ap
38	41.4	2.4	13862	3	US-09-764-891-10204	Sequence 10204, A
39	41.4	2.4	13862	5	US-10-205-428-1003	Sequence 1003, Ap
40	41.2	2.4	1324	9	US-10-450-763-3760	Sequence 3760, Ap
41	41.2	2.4	1845	8	US-10-425-115-120327	Sequence 120327,
42	41.2	2.4	5592	9	US-10-450-763-3762	Sequence 3762, Ap
43	40.8	2.4	15738	6	US-10-329-079-12	Sequence 12, Appl
44	40.8	2.4	37360	6	US-10-329-079-6	Sequence 6, Appl
45	40.6	2.4	600	9	US-10-972-079-71259	Sequence 71259, A

ALIGNMENTS

RESULT 1

US-09-989-890-105
; Sequence 105, Application US/09989890
; Publication No. US20040166105A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Pluta, Jason
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
; FILE REFERENCE: DEX-0287
; CURRENT APPLICATION NUMBER: US/09/989,890
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,509
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-890-105

Query Match 100.0%; Score 1713; DB 3; Length 1713;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCCCGCCCTGGACACCCCGCCAGCATCTGGCCCTCCACGCTTGGAGACCGTGGAG	60
Db	1	ATGCCCGCCCTGGACACCCCGCCAGCATCTGGCCCTCCACGCTTGGAGACCGTGGAG	60
Qy	61	CGGCCACAGAGCTATGTCTGAGACATATGATAACCACTCAGCCCCCACCACCGCG	120
Db	61	CGGCCACAGAGCTATGTCTGAGACATATGATAACCACTCAGCCCCCACCACCGCG	120
Qy	121	CGCACCGTAGACACCCCGCCAGCATCTGGCCCTCCACGCTTGGAGACCGTGGAG	180
Db	121	CGCACCGTAGACACCCCGCCAGCATCTGGCCCTCCACGCTTGGAGACCGTGGAG	180
Qy	181	ATCTCTGGCTCTGCTGAGCGCGCCCTTGGAGTCCCCCAGCTGCTGCTGGCGACCC	240
Db	181	ATCTCTGGCTCTGCTGAGCGCGCCCTTGGAGTCCCCCAGCTGCTGCTGGCGACCC	240
Qy	241	TGGGTGGAGTGGTGGCGGGCTGCTTCTCGCGCGCTGCGGGATTCCTCCAG	300

Db 390 CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCTTGCCTGTCTACTGAGGACTCCACTGAG 449
Qy 361 GGGACTGCTGAAGCCAACTGGGCGCAAGAGACA CAATGGAGTGGCCCGCCAGCCCTGTATCGT 420
Db 450 GGGACTGCTGAAGCCAACTGGGCGCAAGAGACA CAATGGAGTGGCCCGCCAGCCCTGTATCGT 509
Qy 421 GCACCCCGGAGCGGGGATGSCCAGCGGCTCAAGTCAACCATGGGAGCAGCTTCAGC 480
Db 510 GCACCCCGGAGCGGGGATGSCCAGCGGCTCAAGTCAACCATGGGAGCAGCTTCAGC 569
Qy 481 TACCCCGATTTAAGCTCAAGGCGATCCCTGTGTATCCCTACCGGGGCGACCTCCCCA 540
Db 570 TACCCCGATTTAAGCTCAAGGCGATCCCTGTGTATCCCTACCGGGGCGACCTCCCCA 629
Qy 541 GCCCTGTATCGGACTCTCTGTCGAGAGGCGCACTGSCCGATCCCGCACCCATGCGACAC 600
Db 630 GCCCTGTATCGGACTCTCTGTCGAGAGGCGCACTGSCCGATCCCGCACCCATGCGACAC 689
Qy 601 AGCTGCCAGACACTTTGCGAGTACGTAGTCCTGCTGGCTCCGAGGAGTACTATTCTTCCAT 660
Db 690 AGCTGCCAGACACTTTGCGAGTACGTAGTCCTGCTGGCTCCGAGGAGTACTATTCTTCCAT 749
Qy 661 GAGTCGGACCTGGACCTGCGGAGATGGGCACTGGCTCCATGTCGAGCCGAGAAATTGAT 720
Db 750 GAGTCGGACCTGGACCTGCGGAGATGGGCACTGGCTCCATGTCGAGCCGAGAAATTGAT 809
Qy 721 GTCTCATCTTCAAGAGCTGACAGAGCTGTTCAAGGTACACAGATTCGATGAGCTGGCC 780
Db 810 GTCTCATCTTCAAGAGCTGACAGAGCTGTTCAAGGTACACAGATTCGATGAGCTGGCC 869
Qy 781 AAGTCACATCAGACACTGTTCTTGGAGAACCAAGTAAAGTCTCGGACCTTATCAGC 840
Db 870 AAGTCACATCAGACACTGTTCTTGGAGAACCAAGTAAAGTCTCGGACCTTATCAGC 929
Qy 841 AGCATCAGCAGGACTACCACTGGATGAGCAGCTGTCGAGGCGCGCTGGTACGCGGC 900
Db 930 AGCATCAGCAGGACTACCACTGGATGAGCAGCTGTCGAGGCGCGCTGGTACGCGGC 989
Qy 901 ATCATTTGCAATTAGTACCGGAAAGACCGTGTCTGCGCCACAGACCTCGGAGGTCGTTCA 960
Db 990 ATCATTTGCAATTAGTACCGGAAAGACCGTGTCTGCGCCACAGACCTCGGAGGTCGTTCA 1049
Qy 961 ACTCGGGCTGCTGCCCCCAACCGCTGTGCCCCCTGACAGTGGCCATGAGACCATGGTGGC 1020
Db 1050 ACTCGGGCTGCTGCCCCCAACCGCTGTGCCCCCTGACAGTGGCCATGAGACCATGGTGGC 1109
Qy 1021 TCAGGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCAGAGAGACGCTGCAGATGCC 1080
Db 1110 TCAGGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCAGAGAGACGCTGCAGATGCC 1169
Qy 1081 ATGCCCCGGAAGCTGAGGCTTATGGAGCTTCCAGGCTTCCAGGCTACCCAGACCATGACTCATCC 1140
Db 1170 ATGCCCCGGAAGCTGAGGCTTATGGAGCTTCCAGGCTTCCAGGCTACCCAGACCATGACTCATCC 1229
Qy 1141 TTCAGGCGACCGACACAGACTCGTCGGGGGCAACCTTGTCTCAGGTGACTGCTAAACC 1200
Db 1230 TTCAGGCGACCGACACAGACTCGTCGGGGGCAACCTTGTCTCAGGTGACTGCTAAACC 1289
Qy 1201 CTGCGAGGCCAGCTGCCACACCTTTCTGGGAGAGCATGGCCTACAGATCAAGAGGG 1260
Db 1290 CTGCGAGGCCAGCTGCCACACCTTTCTGGGAGAGCATGGCCTACAGATCAAGAGGG 1349
Qy 1261 GGACACGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGGCCCACTGTGCTCTCC 1320
Db 1350 GGACACGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGGCCCACTGTGCTCTCC 1409
Qy 1321 TGCCTTTGGCTGACTGGGTTCTGGACCATGTGCAATTCTACTGGGCCCATGGGATCTCATC 1380
Db 1410 TGCCTTTGGCTGACTGGGTTCTGGACCATGTGCAATTCTACTGGGCCCATGGGATCTCATC 1469
Qy 1381 TCCCTTCATCCCGAGCTGGTCTCATCCCTGCCAGGGCCCTTCTTCTGCTCATGGTCT 1440
Db 1470 TCCCTTCATCCCGAGCTGGTCTCATCCCTGCCAGGGCCCTTCTTCTGCTCATGGTCT 1529

Qy 1441 TCAGGTGGCCTGTATCATGGAAGCTAAGGAGTTAAGGATTAACCTTCTGGGAGTGAACCCCTG 1500
Db 1530 TCAGGTGGCCTGTATCATGGAAGCTAAGGAGTTAAGGATTAACCTTCTGGGAGTGAACCCCTG 1589
Qy 1501 ACTCCATCCCTTATTGGCCACCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAT 1560
Db 1590 ACTCCATCCCTTATTGGCCACCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAT 1649
Qy 1561 TCAACAGTTAAAGAGAGCTTATCTTAAATGATTTGTTATTTGGGGGTGGGAGGCCCACT 1620
Db 1650 TCAACAGTTAAAGAGAGCTTATCTTAAATGATTTGTTATTTGGGGGTGGGAGGCCCACT 1709
Qy 1621 CTATGTTATGTTAAGAGTGGTCTGGTCTTGGCTGATGTTCTGTATCTTAACATGAC 1680
Db 1710 CTATGTTATGTTAAGAGTGGTCTGGTCTTGGTCTTGGTCTGATGTTCTGTATCTTAACATGAC 1769
Qy 1681 CACAGTTTGTAGTAC 1696
Db 1770 CACAGTTTGTAGTAC 1785

RESULT 3

US-09-989-920-56
; Sequence 56, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chonghua
; FILE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-56

Query Match 93.5%; Score 1602.4; DB 3; Length 1977;
Best Local Similarity 99.0%; Pred.No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 11; Gaps 9;

Qy 1 ATGCCCGCCCTGGACACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACCGTGGAG 60
Db 254 ATGCCCGCCCTGGACACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACCGTGGAG 313
Qy 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCGCCACCAAGCCGC 120
Db 314 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCGCCACCAAGCCGC 373
Qy 121 CGCACCGGTAGACACACCCAGGACCTGGCCACCATGGGCGCAGAGCATTTACCTTC 180
Db 374 CGCACCGGTAGACACACCCAGGACCTGGCCACCATGGGCGCAGAGCATTTACCTTC 433
Qy 181 ATCTCTGGCTCTGCTGAGCGCGCTTGTAGTCCGCCACCTGTCTGCTCTGCGGACCC 240
Db 434 ATCTCTGGCTCTGCTGAGCGCGCTTGTAGTCCGCCACCTGTCTGCTCTGCGGACCC 493
Qy 241 TGGGTGTGGAGTGTGGTGGCGGTGCTTCTGCTTCGG-CCGCTGCCGGATTTGCCTCCA 299
Db 494 TGGGTGTGGAGTGTGGTGGCGGTGCTTCTGCTTCGGCCGCTGCGGGATTTGCCTCCA 553
Qy 300 GGCCTGTGGA-CCCTGTGTGGGGATGAGCCCGCTGCTGTCTACTGAGGACT-CCACT 357
Db 554 GGCCTGTGGAGGCTGTGTGGGGATGAGCCCGCTGCTGTCTACTGAGGACTTCCACT 613

QY 358 GAGGGACTGCTGAAGCCAACTGG-GCCAAAGGAGCACAATGAGTGGCCCGCCCGAGCCCTCA 416
Db 614 GAGGGACTGCTGAAGCCAACTGGTGGCCAAAGAGCACAATGAGTGGCCCGCCCGAGCCCTGA 673
QY 417 TCGTGACACCCCGCAG-CCGGCGGGATGGCCA---GGGGCTCAAGTCAACATCAATGGGCAGCA 472
Db 674 TCGTGACACCCCGCAGACCGCGGGATGGCCAGCGGGCTGCAAGTCAACATGGGCAGCA 733
QY 473 GCTTCAGCTACCCCGAGTGAAGCTCAAGAGGATCCCTGTGTATCCCTAACCGAG-GGCC 531
Db 734 GCTTCAGCTACCCCGAGTGAAGCTCAAGAGGATCCCTGTGTATCCCTAACCGAGAGGCC 793
QY 532 ACCTCCCGAGCCCTGATCGGACTCCTGCTCAAGGAGCAGCTGCCCGCATCCCGCACCC 591
Db 794 ACCTCCCGAGCCCTGATCGGACTCCTGCTCAAGGAGCAGCTGCCCGCATCCCGCACCC 853
QY 592 ATGCGA-CACAGCCTGCCAGCACCTTTTGCCAGTAGTCTCGTGGCTCCGAGGAGTACTA 650
Db 854 ATGCGAGCACGCTGCCAGCACCTTTTGCCAGTAGTCTCGTGGCTCCGAGGAGTACTA 913
QY 651 TTCCTTCCATGAGTCGGACCTGGAACCTGCCGAGATGGGCGAGTGGCTCCATGTCGAGCGG 710
Db 914 TTCCTTCCATGAGTCGGACCTGGAACCTGCCGAGATGGGCGAGTGGCTCCATGTCGAGCGG 973
QY 711 AGAATTTGATGTGCTCATCTTCAAGAGCTGACAGA-GCTGTTTCAGCGTACACCCAGATCG 769
Db 974 AGAATTTGATGTGCTCATCTTCAAGAGCTGACAGAGGCTGTTTCAGCGTACACCCAGATCG 1033
QY 770 ATGAGTGGCCAAAGTGCACATCAGACATGTGTCTCTGGAGAGACCACTAAGATCTCGG 829
Db 1034 ATGAGTGGCCAAAGTGCACATCAGACATGTGTCTCTGGAGAGACCACTAAGATCTCGG 1093
QY 830 ACCTTATCAGCAGCATCA CGAGGACTACCACTGGATGAGCAGGATGCTGAGGGCGGCC 889
Db 1094 ACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGGCGGCC 1153
QY 890 TGGTAGCGCGCATATTCGCATTTAGTACCGGAAGAGCGTGTCTGCCCCACAGACCTCGG 949
Db 1154 TGGTAGCGCGCATATTCGCATTTAGTACCGGAAGAGCGTGTCTGCCCCACAGACCTCGG 1213
QY 950 AGGGTCGTTCAACTCGGGTGTGTCGCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGA 1009
Db 1214 AGGGTCGTTCAACTCGGGTGTGTCGCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGA 1273
QY 1010 CCATGTTGGGCTCAGTCTCAGCCAGATGAGCTGACAGTGCAAGTCTCCAGGAGACGA 1069
Db 1274 CCATGTTGGGCTCAGGCTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGA 1333
QY 1070 CTGCAGATGCCATCGCCCGGAGCTGAGGCCCTTATGGAGCTCCAGGGTACCAGCAAGCC 1129
Db 1334 CTGCAGATGCCATCGCCCGGAGCTGAGGCCCTTATGGAGCTCCAGGGTACCAGCAAGCC 1393
QY 1130 ATGACTCATCTTCCAGGGCACCGACACAGACTCGTGGGGGACACCTTTGCTCCAGGTGT 1189
Db 1394 ATGACTCATCTTCCAGGGCACCGACACAGACTCGTGGGGGACACCTTTGCTCCAGGTGT 1453
QY 1190 ACTGCTAAACCCCTGCCAGGCCAGCTGCCACACCTTTCTGGGAGAGCATGSCCTACAG 1249
Db 1454 ACTGCTAAACCCCTGCCAGGCCAGCTGCCACACCTTTCTGGGAGAGCATGSCCTACAG 1513
QY 1250 AATGAAGGGGGACCAAGNACCCCTGTGGGAGAGGCTTAGACCTGAAGCATGGCCACT 1309
Db 1514 AATGAAGGGGGGACCAAGNACCCCTGTGGGAGAGGCTTAGACCTGAAGCATGGCCACT 1573
QY 1310 CTGGCTCCTCTGCTGCTGACTGGGTTCTTGAGCCATGTGCAATTTCACTGGGCGCATG 1369
Db 1574 CTGGCTCCTCTGCTGCTGACTGGGTTCTTGAGCCATGTGCAATTTCACTGGGCGCATG 1633
QY 1370 GGATCTACATCTCCTTTGCAATCCCGACGTGTTGATCCCTGCCAGGGCGCCTTCCTTCCT 1429
Db 1634 GGATCTACATCTCCTTTGCAATCCCGACGTGTTGATCCCTGCCAGGGCGCCTTCCTTCCT 1693

RESULT 4

US-09-989-920-117
; Sequence 117, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989, 920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-117

Query Match 93.5%; Score 1602.4; DB 3; Length 1977;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 11; Gaps 9;

QY 1 ATGCCCGCGCCCTGGACACCCCGCCAGCATCTGGGCTTCCACGCTTGGGACCGTGGGAG 60
Db 254 ATGCCCGCGCCCTGGACACCCCGCCAGCATCTGGGCTTCCACGCTTGGGACCGTGGGAG 313
QY 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCTCAGCCCCCACAAGCCGC 120
Db 314 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCTCAGCCCCCACAAGCCGC 373
QY 121 CGACCCGTAGACCAGACCCCGAGGCCCTGGCCACCATGGGCGAGAGCATTAACCTTC 180
Db 374 CGACCCGTAGACCAGACCCCGAGGCCCTGGCCACCATGGGCGAGAGCATTAACCTTC 433
QY 181 ATCTCTGGCTCTGTCTGAGCGCGCCCTTGTAGTCCCGCAGCTGTGCTGTCTGGCGACCC 240
Db 434 ATCTCTGGCTCTGTCTGAGCGCGCCCTTGTAGTCCCGCAGCTGTGCTGTCTGGCGACCC 493
QY 241 TGGGTGTGGAGTGTGTGCGGGCTGCTTCTGCTTCG-CGCGTCCGGGATTTGCTTCCA 299
Db 494 TGGGTGTGGAGTGTGTGCGGGCTGCTTCTGCTTCGCGCGGCTGCTGCGGATTTGCTTCCA 553
QY 300 GCGCTGTGGA-GCCTGTGTGCGGGATGAGCCCGCTGCTGTCTACTGAGGACT-CCACT 357
Db 554 GCGCTGTGAGGCTGTGTGCGGGGATGAGCCCGCTGCTGTCTACTGAGGACTTCCCACT 613

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QY 358 GAGGGAGTCTGCTGAGCCAACTGG-GCCAGAGGACCAATGGAGTGCCTCCCGCCGACCTGA 416
Db 614 GAGGGAGTCTGCTGAGCCAACTGGTCCAGAGGACCAATGGAGTGCCTCCCGCCGACCTGA 673
QY 417 TCGTGACACCCCGCCAG-CCGCGGGATGGCCA---GCGGCTCAAGTCAACCATGGGAGCA 472
Db 674 TCGTGACACCCCGCCAGACCGGCGGGATGGCCAGCGGGCTGCAAGTCAACCATGGGAGCA 733
QY 473 GCTTCAGTACCCCGATGTTAAGTCAAGGCAATCCCTGTGTATCCCTACCCAG-GGCC 531
Db 734 GCTTCAGTACCCCGATGTTAAGTCAAGGCAATCCCTGTGTATCCCTACCCAGAGGCC 793
QY 532 ACCTCCCGACCCCTGATCGGACTCTGTGTGCAAGAGCCACTGGCCGATCCCGCCACCC 591
Db 794 ACCTCCCGACCCCTGATCGGACTCTGTGTGCAAGAGCCACTGGCCGATCCCGCCACCC 853
QY 592 ATGCGA-CACAGCTGCCAGCACCTTTGCGAGTAGTCTCGTGGCTCCGAGGAGTACTA 650
Db 854 ATGCGAGCACGCTGCCAGCACCTTTGCGAGTAGTCTCGTGGCTCCGAGGAGTACTA 913
QY 651 TTCTTTCCATGATCGGACCTGACCTGCGCGAGATGGGCAAGTGGCTCCATGTGAGCGG 710
Db 914 TTCTTTCCATGATCGGACCTGCGACCTGCGCGAGATGGGCAAGTGGCTCCATGTGAGCGG 973
QY 711 AGAAATTGATGTGCTCATCTTCAAGAGCTGACAGA-GCTGTTTCAGGCTACACCATCG 769
Db 974 AGAAATTGATGTGCTCATCTTCAAGAGCTGACAGAGGCTGTTTCAGGCTACACCATCG 1033
QY 770 ATGAGCTGGGCAAGTGCACATCAGACACTGTGTTCTCGGAGAGACCAAGTAAGATCTCGG 829
Db 1034 ATGAGCTGGGCAAGTGCACATCAGACACTGTGTTCTCGGAGAGACCAAGTAAGATCTCGG 1093
QY 830 ACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGGCGCC 889
Db 1094 ACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGGCGCC 1153
QY 890 TGGTACGGGCAATCTCGGATAGTACCCGAAAGACCGTGTGCGCCACAGACCTCGG 949
Db 1154 TGGTACGGGCAATCTCGGATAGTACCCGAAAGACCGTGTGCGCCACAGACCTCGG 1213
QY 950 AGGGTCGTTCAACTCGGGCTGTCGCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGA 1009
Db 1214 AGGGTCGTTCAACTCGGGCTGTCGCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGA 1273
QY 1010 CCAATGGTGGGCTCAGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCAGGAGACGA 1069
Db 1274 CCAATGGTGGGCTCAGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCAGGAGACGA 1333
QY 1070 CTGCAGATGCGATCGCCCGGAGCTGAGGCTTATGAGCTCAGGGTACCCAGCAAGCC 1129
Db 1334 CTGCAGATGCGATCGCCCGGAGCTGAGGCTTATGAGCTCAGGGTACCCAGCAAGCC 1393
QY 1130 ATGACTCATCTTCCAGGGGACCGACACAGACTCGTGGGGGACCCCTTGTCCAGGTGT 1189
Db 1394 ATGACTCATCTTCCAGGGGACCGACACAGACTCGTGGGGGACCCCTTGTCCAGGTGT 1453
QY 1190 ACTGTCTAACCCCTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGGCCTACAG 1249
Db 1454 ACTGTCTAACCCCTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGGCCTACAG 1513
QY 1250 AATGAAGAGGGGACAGAGAACCCCTGTGGGAGAGGCTTAGACCTGAAGAGTGCCCACT 1309
Db 1514 AATGAAGAGGGGACAGAGAACCCCTGTGGGAGAGGCTTAGACCTGAAGAGTGCCCACT 1573
QY 1310 CTGGCTCTCTCGCTGCTGCTGAGTGGTTCTGGACCATGTGCAATTTCACTGGGGCATTG 1369
Db 1574 CTGGCTCTCTCGCTGCTGCTGAGTGGTTCTGGACCATGTGCAATTTCACTGGGGCATTG 1633
QY 1370 GGAATCTACATCTCTTGCATPCCCGAGTGGTCTGATCCCTGCGAGGGCCCTTCTTCTCT 1429
Db 1634 GGAATCTACATCTCTTGCATPCCCGAGTGGTCTGATCCCTGCGAGGGCCCTTCTTCTCT 1693
QY 1430 GCTCATGGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCAATTACCTTCTGGG 1489
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Db 1694 GCTCATGGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGG 1753
QY 1490 AGTGAACCCCTGACTCCATCCCCCTATTGGCACCCCTAAACCAATCATGCAAACTTCTCCCTC 1549
Db 1754 AGTGAACCCCTGACTCCATCCCCCTATTGGCACCCCTAAACCAATCATGCAAACTTCTCCCTC 1813
QY 1550 CTGGGGTAAATCAACAGTTAAAGAGCTTATCTTAAATGATATTGTTATTTGGGGGGTGGG 1609
Db 1814 CTGGGGTAAATCAACAGTTAAAGAGCTTATCTTAAATGATATTGTTATTTGGGGGGTGGG 1873
QY 1610 CAGGGCCCACTCTATGTTTAAAGAGTGGTCTTGGTTCTTGGCTGATGTTCTGTAT 1669
Db 1874 CAGGGCCCACTCTATGTTTAAAGAGTGGTCTTGGTTCTTGGCTGATGTTCTGTAT 1933
QY 1670 CTTAAACATGACCACAGTTTGTAGTACCTCGCGCGGACCCACGC 1713
Db 1934 CTTAAACATGACCACAGTTTGTAGTACCTCGCTCGGACCCACGC 1977
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RESULT 5

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US-10-074-475-124
; Sequence 124, Application US/10074475
; Publication No. US20030092898A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Karra, Kalpana
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
; TITLE OF INVENTION: Genes and Proteins
; FILE REFERENCE: DEX-0313
; CURRENT APPLICATION NUMBER: US/10/074,475
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,292
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-074-475-124
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Query Match 35.5%; Score 607.6; DB 5; Length 654;
Best Local Similarity 96.6%; Pred. No. 5.le-178;
Matches 632; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 89 ATGATAAACACACTCAGCCGCCACCAAGCGCGCGACCCGTAGACACAGACCCCAAGGACC 148
Db 1 ATGATAAACACACTCAGCCGCCACCAAGCGCGCGACCCGTAGACACAGACCCCAAGGACC 60
QY 149 CTGGCCACCATGGGCGCAGAGAGCATTTACCTTCACTCTTGGCTCTGTGAGCGCGCCCTTG 208
Db 61 CTGGCCACCATGGGCGCAGAGAGCATTTACCTTCACTCTTGGCTCTGTGAGCGCGCCCTTG 120
QY 209 AGTCCCGCCACCTGCTGCTGCTGCTGCGGACCCCTGGGTGTGGGAGTGGTGC CGGGCTGCCT 258
Db 121 AGTCCCGCCACCTGCTGCTGCTGCTGCGGACCCCTGGGTGTGGGAGTGGTGC CGGGCTGCCT 180
QY 269 TCTGCTTCCGCGCGCTGCGCGGATTCCTCCAGCGCTGTGAGGCTCTGTGTCGCGGATGCA 328
Db 181 TCTGCTTCCGCGCGCTGCGCGGATTCCTCCAGCGCTGTGAGGCGCGTGTGCGGGAGTGA 240
QY 329 GCCCTGCTGCTGCTACTGAGGAGCTCCACTGAGGGAGCTGCTGAAGCAAACTGGGCCAAGG 388
Db 241 GCCCTGCTGCTGCTACTGAGGAGCTCCCTGAGGGAGTCTGCTGAAGCAAACTGCTCCAGG 300
QY 389 AGCACAATGGAGTGGCCCCCAGCCCTGATCGTGCACCCCCCAGCCCGGGGAGTGGCCA-- 446
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301	Db	 AGCAAAATGGAGTGGCCCCCAAGCCCTGATCGTGCAGCCCCCGCCGCGGATGGCCAGG	360
447	QY	-GGGGTCAAGTCAACCATGGGCGAGCAGCTTCAGCTACCCCGATGTTTAAGCTCAAAAGGCA	505
361	Db	CGGGTGCNAGTCAACCAATGGGCGAGCAGCTTCAGCTACCCGATGTTTAAGCTCAAAAGCA	420
506	QY	TCCCTGTGTATCCCTACCCGAGGGGCCACCTCCCCAGCCCCCTGATCGGAATCTCTGCTGCA	565
421	Db	TCCCTGTGTATCCCTACCCGAGAGGCCACCTCCCCAGGCCCTGATGCGGAATCTCTGCTGCA	480
566	QY	AGGAGCCACTGGCCGATCCCCCAACCCATGCGACACAGCCTGCCCAGCAGCACTTTGGCCAGTA	625
481	Db	AGGAGCCACTGGCCGATCCCCCAACCCAGCGAGCACAGCCTGCCCAGCAGCACTTTGGCCAGTA	540
626	QY	GTCTCTGTGGCTCGAGGAGTACTATTCTTTCCATGATCGGACCTGGACCTGCCCGAGA	685
541	Db	GTCTCTGTGGCTCGAGGAGTACTATTCTTTCCATGATCGGACCTGGACCTGCCCGAGA	600
686	QY	TGGGCAAGTGGCTCCCATGTGCGAGCCGAGAAAATTGATGTGCTCATCTTCAAGAAGC	739
601	Db	TGGGCAAGTGGCTCCCATGTGCGAGCCGAGAAAATTGATGTGCTCATCTTCAAGAAGC	654

RESULT. 6

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US-10-779-543-5731
; Sequence 5731, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5731
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 15, 16, 17, 18, 20,
; LOCATION: 22, 23, 24, 25, 28, 29, 30, 36, 41, 85, 89, 97, 106, 108,
; LOCATION: 115, 134, 139, 177, 185, 207, 232, 275, 283, 303, 320, 32
; LOCATION: 356, 414, 451, 469, 551, 566, 582, 588, 591, 605, 631, 65
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 661, 678, 681, 687, 689, 702, 706, 710, 711, 713, 722
; OTHER INFORMATION: n = A,T,C or G

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US-09-989-920-55		Query Match 22.5%; Score 385; DB 3; Length 385; Best Local Similarity 100.0%; Pred. No. 8e-109; Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1190	ACTGCTAAACCCCTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGGCCTACAG	1249
Db	1	ACTGCTAAACCCCTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGGCCTACAG	60
Qy	1250	AATGAAGAGGGGGACACAGGAACCCCTCTGGAGAGGCTTAGACCTGAAGCAGTGCCCACT	1309
Db	61	AATGAAGAGGGGGACACAGGAACCCCTCTGGAGAGGCTTAGACCTGAAGCAGTGCCCACT	120
Qy	1310	CTGGCTCCTCTCTGCTTTGGCTGACTCGGTTCCTGGACCATGTGCAATTTCACTGGGCAATG	1369
Db	121	CTGGCTCCTCTCTGCTTTGGCTGACTCGGTTCCTGGACCATGTGCAATTTCACTGGGCAATG	180
Qy	1370	GGATCTACATCTCTTTCATCCCGACGCTGCTGATCCCTGCCAGGCCCCCTTCTTCCT	1429
Db	181	GGATCTACATCTCTTTCATCCCGACGCTGCTGATCCCTGCCAGGCCCCCTTCTTCCT	240
Qy	1430	GCTCATCGTCTTCAGGTGGCTGATCATGGAAGTAGAGGATTAGGCATTACCTTTCTGGG	1489
Db	241	GCTCATCGTCTTCAGGTGGCTGATCATGGAAGTAGAGGATTAGGCATTACCTTTCTGGG	300
Qy	1490	AGTGAACCCCTGACTCCATCCCTTATTGCCACCCCTAACCAATCATGCAAACTTCTCCCTC	1549
Db	301	AGTGAACCCCTGACTCCATCCCTTATTGCCACCCCTAACCAATCATGCAAACTTCTCCCTC	360
Qy	1550	CTGGGGTAAATTCACAGTTAAAAG	1574
Db	361	CTGGGGTAAATTCACAGTTAAAAG	385
RESULT 8			
US-09-989-890-104			
; Sequence 104, Application US/09989890			
; Publication No. US20040166105A1			
; GENERAL INFORMATION:			
; APPLICANT: Salceda, Susana			
; APPLICANT: Macina, Roberto			
; APPLICANT: Recipon, Herve			
; APPLICANT: Pluta, Jason			
; APPLICANT: Sun, Yongming			
; APPLICANT: Liu, Chenghua			
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and			
; FILE REFERENCE: DEX-0287			
; CURRENT APPLICATION NUMBER: US/09/989,890			
; CURRENT FILING DATE: 2001-11-21			
; PRIOR APPLICATION NUMBER: 60/252,509			
; PRIOR FILING DATE: 2000-11-22			
; NUMBER OF SEQ ID NOS: 280			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 104			
; LENGTH: 386			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-989-890-104			
Query Match 22.2%; Score 380.2; DB 3; Length 386;			
Best Local Similarity 99.2%; Pred. No. 2.5e-107;			
Matches 382; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
Qy	1196	AACCCCTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGGCCTACAGAAATGAA	1255
Db	2	ACCCCTGGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGGCCTACAGAAATGAA	61
Qy	1256	GAGGGGACACAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCT	1315
Db	62	GAGGGGACACAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCT	121
Qy	1316	CTCTCTGCTTGGCTGACTGGGTTCCTGGACCATGTGCAATTTCACTGGGCCATGGGATCT	1375

Db	122	CCCTCTGCCTTGGCTGACTGGGTCTCTGGACCAATGTGCATTTCACTGGGCCAATGGGA	181
Qy	1376	ACATCTCTTTGCAATCCCCAGCTGGTCTGTGATCCCTGCCAGGGGCCCTTCTCTTCTGCTCAT	1435
Db	182	ACATCTCTTGTGATCCCCAGCTGGTCTGTGATCCCTGCCAGGGGCCCTTCTCTTCTGCTCAT	241
Qy	1436	GGTCTTCAGTGGCCCTGATCATGAGAAAGTAAAGAGTTAGGCATTACCTTCTGGAGTGAA	1495
Db	242	GGTCTTCAGTGGCCCTGATCATGAGAAAGTAAAGAGTTAGGCATTACCTTCTGGAGTGAA	301
Qy	1496	CCCTGACTCCATCCCCCTATTGTGCACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGG	1555
Db	302	CCCTGACTCCATCCCCCTATTGTGCACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGG	361
Qy	1556	GTAATTCAACAGTTAAAAAGAGCTT	1580
Db	362	GTAATTCAACAGTTAAAAAGAGCTT	386
RESULT 9			
US-10-074-475-123			
; Sequence 123, Application US/10074475			
; Publication No. US20030092898A1			
; GENERAL INFORMATION:			
; APPLICANT: Salceda, Susana			
; APPLICANT: Macina, Roberto			
; APPLICANT: Hu, Ping			
; APPLICANT: Recipon, Herve			
; APPLICANT: Karra, Kalpana			
; APPLICANT: Caferkey, Robert			
; APPLICANT: Sun, Yongming			
; APPLICANT: Liu, Chenghua			
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific			
; FILE REFERENCE: DEX-0313			
; CURRENT APPLICATION NUMBER: US/10/074,475			
; CURRENT FILING DATE: 2002-02-13			
; PRIOR APPLICATION NUMBER: 60/268,292			
; PRIOR FILING DATE: 2001-02-13			
; NUMBER OF SEQ ID NOS: 295			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 123			
; LENGTH: 386			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-10-074-475-123			
Query Match 22.2%; Score 380.2; DB 5; Length 386;			
Best Local Similarity 99.2%; Pred. No. 2.5e-107;			
Matches 382; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
Qy	1196	AACCCCTGCCAGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGCCCTACAGAAATGAA	1255
Db	2	ACCCCTGGCCAGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGCCCTACAGAAATGAA	61
Qy	1256	GAGGGGACACAGAAACCCCTGTGGGAGAGCTTTAGACCTGAAGCAGTGGCCACTCTGGCT	1315
Db	62	GAGGGGACACAGAAACCCCTGTGGGAGAGCTTTAGACCTGAAGCAGTGGCCACTCTGGCT	121
Qy	1316	CCTCCTGCCTTGGCTGACTGGGTTCTTGGACCAATGTGCATTTCACTGGGCCATGGGA	1375
Db	122	CCTCCTGCCTTGGCTGACTGGGTTCTTGGACCAATGTGCATTTCACTGGGCCATGGGA	181
Qy	1376	ACATCTCTTGCATCCCCAGCTGGTCTGTGATCCCTGGCAGGGGCCCTTCTCTGCTCAT	1435
Db	182	ACATCTCTTGCATCCCCAGCTGGTCTGTGATCCCTGGCAGGGGCCCTTCTCTGCTCAT	241
Qy	1436	GGTCTTCAGTGGCCCTGATCATGAGAAAGTAAAGAGTTAGGCATTACCTTCTGGAGTGAA	1495
Db	242	GGTCTTCAGTGGCCCTGATCATGAGAAAGTAAAGAGTTAGGCATTACCTTCTGGAGTGAA	301
Qy	1496	CCCTGACTCCATCCCCCTATTGTGCACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGG	1555

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Db 302 CCTGACTCCATCCCTATTGTCACCCCTAAACCAATCATGCAACTTCTCCCTCCCTGGG 361
QY 1556 GTAATTCACAGTTAAAGAAGCTT 1580
Db 362 GTAATTCACAGTTAAAGAAGCTT 386

RESULT 10
US-10-779-543-10096
; Sequence 10096, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10096
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 355
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-10096

Query Match 20.6%; Score 352.6; DB 9; Length 393;
Best Local Similarity 98.4%; Pred. No. 9.8e-99;
Matches 366; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 805 CTGGAGAACACAGTAAGATCTCGGACCTTATCAGCAGCATCAGCAGACTACCACTG 864
Db 21 CTGGAGAACACAGTAAGATCTCGGACCTTATCAGCAGCATCAGCAGACTACCACTG 80

QY 865 GATGACAGATGCTCAGGCGCCCTGGTACGGGCATCATTCGCATTAGTACCCGAAAG 924
Db 81 GATGACAGATGCTCAGGCGCCCTGGTACGGGCATCATTCGCATTAGTACCCGAAAG 140

QY 925 AGCCGTGCTCGCCACAGACCTCGGAGGGTGGTTCAACTCGGCTCTGCCCCCAACCGCT 984
Db 141 AGCCGTGCTCGCCACAGACCTCGGAGGGTGGTTCAACTCGGCTCTGCCCCCAACCGCT 200

QY 985 GCTGCCCTCTGACAGTGGCCATGACATGCTGGGCTCAGGCTCAGCCAGGATGAGCTG 1044
Db 201 GCTGCCCTCTGACAGTGGCCATGACATGCTGGGCTCAGGCTCAGCCAGGATGAGCTG 260

QY 1045 ACAGTGCAGATCTCCCAAGGAGACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCCTTAT 1104
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Db 261 ACAGTGCAGATCTCCCAAGGAGACGACTGCAGATGCCATGCCCGAAGCTGAGCCCTTAT 320
QY 1105 GGAGCTCCAGGTACCCAGCAAGCCATGACTCATCTTCCA-GGGCACCAGACACAGACTC 1163
Db 321 GGAGCTCCAGGTACCCAGCAAGCCATGACTCATCTTCCAAGGGGACCGACACAGACTC 380
QY 1164 GTCGGGGGCACC 1175
Db 381 GTCGGGGGCACC 392

RESULT 11
US-10-779-543-12051
; Sequence 12051, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12051
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 401
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-12051

Query Match 20.3%; Score 347; DB 9; Length 427;
Best Local Similarity 99.7%; Pred. No. 5.6e-97;
Matches 347; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCCCGCCCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACCGTGGGAG 60
Db 80 ATGCCCGCCCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACCGTGGGAG 139

QY 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACTCAGCCCCCAACGACCGC 120
Db 140 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACTCAGCCCCCAACGACCGC 199

QY 121 CGCACCCGTAGACACCCCGCCAGGACCTGGCCACCATGGGCCAGAGACATTACCTTC 180
Db 200 CGCACCCGTAGACACCCCGCCAGGACCTGGCCACCATGGGCCAGAGACATTACCTTC 259

QY 181 ATCTCTGGCTCTGCTGAGCGCGGCCCTTGTAGTCCCCCACCCTGTGCTCTGGCGACCC 240
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Db      260 ATCTCTGGCTCTGCTGAGCGCGGCGCTTGAGTCCCCACCTGCTGCTGCTCTGGGAGCC 319
Qy      241 TGGGTGTGGGAGTGTGTGCGGCGTGCCTTCTGCTTCCGCGCTGCGGGATTGCCTCCAG 300
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Db      380 CGCTGTGAGAGCTGTGTGCGGNGATGACGCCCTGCCTGTCTACTAG 427

RESULT 12
US-10-779-543-1705
; Sequence 1705, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1705
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-779-543-1705

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	Query Match	17.5%	Score 300;	DB 9;	Length 300;
	Best Local Similarity	100.0%;	Pred. No. 2.1e-82;		
	Matches 300;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	825	CTCGGACCTTTATCAGCAGCATCAGCAGGACTACACCTGGATGAGCAGGATGCTGAGGG	884		
Db	1	CTCGGACCTTTATCAGCAGCATCAGCAGGACTACACCTGGATGAGCAGGATGCTGAGGG	60		
Qy	885	CCGGCTGGTACGCGGCATCATTTGCATTAGTACCGGAAAGCCGCTGCTGCCACAGAC	944		
Db	61	CCGGCTGGTACGCGGCATCATTTGCATTAGTACCGGAAAGCCGCTGCTGCCACAGAC	120		
Qy	945	CTCGGAGGGTCGTTCAACTCGGGCTGTGCCCCCAACCGCTGCTGCCCTGCACAGTGGCCA	1004		
Db	121	CTCGGAGGGTCGTTCAACTCGGGCTGTGCCCCCAACCGCTGCTGCCCTGCACAGTGGCCA	180		
Qy	1005	TGAGACCATGGTGGGCTCAGGTCACGCCAGGATGAGCTGACAGTGCAGATCTCCAGGA	1064		
Db	181	TGAGACCATGGTGGGCTCAGGTCACGCCAGGATGAGCTGACAGTGCAGATCTCCAGGA	240		
Qy	1065	GACGACTGCAGATGCCATCGCCCCGGGAAGCTGAGGCGCTTATGGAGCTCCAGGGTACCCAGC	1124		

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Db      241  GACGACTGCGAGATGCCATCGCCCGGAAGCTGAGGCGCTTATGGAGCTCCAGGGTACCCAGC 300
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US-10-076-555-34
; Sequence 34, Application US/10076555
; Publication No. US20030065156A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominiguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Novel Human Genes and Gene Expression
; TITLE OF INVENTION: Products I
; FILE REFERENCE: 2300-1480
; CURRENT APPLICATION NUMBER: US/10/076,555
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,877
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-555-34

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Query Match	17.4%	Score 298.4	DB 5	Length 300
Best Local Similarity	99.7%	Pred. No. 6.6e-82		
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Qy	800	TGTTCTCGGAGAGAGACGAGTAAGATTCGGAACCTTATCAGGAGCATCACGGAGGACTACC	859	
Db	61	TGTTCTCGGAGAGAGACGAGTAAGATTCGGAACCTTATCAGGAGCATCACGGAGGACTACC	120	
Qy	860	ACCTCGATGAGCAGGATGCTGAGGGCGCCTGGTACGCGGCATCATTCGATAGTATACCC	919	
Db	121	ACCTCGATGAGCAGGATGCTGAGGGCGCCTGGTACGCGGCATCATTCGATAGTATACCC	180	
Qy	920	GAAGAAGCCGTGTCGCCCAACAGACTCGAGGGTCTGTTCAACTCGGGCTGTGCCCCAA	979	
Db	181	GAAGAAGCCGTGTCGCCCAACAGACTCGAGGGTCTGTTCAACTCGGGCTGTGCCCCAA	240	

QY 980 CGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGCTCAGGTCTCAGCCAGGATG 1039
Db 241 CGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGCTCAGGTCTCAGCCAGGATG 300

RESULT 14
US-10-779-543-34
; Sequence 34, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALY EXPRESSED
; FILE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-779-543-34

Query Match 17.4%; Score 298.4; DB 9; Length 300;
Best Local Similarity 99.7%; Pred. No. 6.6e-82;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGACAGAGCTGTTACGGGTACACAGATCGATGAGTGGCCAGTGCACATCAGACACTG 799
Db 1 TGACAGAGCTGTTACGGGTACACAGATCGATGAGTGGCCAGTGCACATCAGACACTG 60

QY 800 TGTTCCTGGAGAGACAGTAAGATCTCGGACCTTATCAGCAGCATCAGCCAGGACTACC 859
Db 61 TGTTCCTGGAGAGACAGTAAGATCTCGGACCTTATCAGCAGCATCAGCCAGGACTACC 120

QY 860 ACCTGATGAGCAGGATGCTGAGGGCCGCTGTGTACCGGCGATCATCGCATTTAGTACC 919
Db 121 ACCTGATGAGCAGGATGCTGAGGGCCGCTGTGTACCGGCGATCATTCGCATTATTACC 180

QY 920 GAAGAGCGGTGCTCGGCCACAGACTCGGAGGCTGTTCACTCGGGCTGCGCCCAA 979
Db 181 GAAGAGCGGTGCTCGGCCACAGACTCGGAGGCTGTTCACTCGGGCTGCGCCCAA 240

QY 980 CGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGCTCAGGTCTCAGCCAGGATG 1039
Db 241 CGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGCTCAGGTCTCAGCCAGGATG 300

; Sequence 116, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Proteins
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 116
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-116

Query Match 7.0%; Score 120; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.6e-26;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1635 GGAGTTGGTTCCTGGTTCCTGGCTGATGTTCTGTATCTTAACATGACACAGTTTGAAGT 1694
Db 60 GGAGTTGGTTCCTGGTTCCTGGCTGATGTTCTGTATCTTAACATGACACAGTTTGAAGT 1

Search completed: March 11, 2006, 22:42:56
Job time : 1289 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 20:00:54 ; Search time 591 Seconds
(without alignments)
6687.647 Million cell updates/sec

Title: US-09-989-890-105

Perfect score: 1713
Sequence: 1 atgccccgcctggacaccc.....tactcggcgagaccacgc 1713

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- Published Applications NA_New.*
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 - 2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq.*
 - 3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq.*
 - 4: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq.*
 - 5: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.*
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 - 10: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq2.*
 - 11: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq3.*
 - 12: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq4.*
 - 13: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1592.8	98.8	1785	9	US-11-072-512-799 Sequence 799, App
2	40.6	2.4	1738	7	US-10-501-035-144 Sequence 144, App
3	40.4	2.4	3320	12	US-11-124-368A-154 Sequence 154, App
4	40.4	2.4	3338	12	US-11-124-368A-156 Sequence 156, App
5	40.4	2.4	3422	12	US-11-124-368A-155 Sequence 155, App
6	38.6	2.3	587	6	US-09-925-065A-893863 Sequence 893863, App
7	38.6	2.3	590	6	US-09-925-065A-894029 Sequence 894029, App
8	38.6	2.3	5706	12	US-11-052-554A-519 Sequence 519, App
9	37.8	2.2	15234	12	US-11-136-527-306 Sequence 306, App
10	37.6	2.2	1431	9	US-11-096-568A-22110 Sequence 22110, App
11	37.6	2.2	38239	7	US-10-330-773-603 Sequence 603, App
12	37.4	2.2	37507	8	US-10-522-037-2 Sequence 2, Appl
13	37.2	2.2	1067	6	US-09-925-065A-551694 Sequence 551694, App
14	37.2	2.2	162173	12	US-11-121-086-72 Sequence 72, Appl
15	37	2.2	6034	7	US-10-501-035-200 Sequence 200, App
16	36.6	2.1	566	6	US-09-925-065A-732134 Sequence 732134, App
17	36.6	2.1	656	6	US-09-925-065A-56292 Sequence 56292, App
18	36.4	2.1	2859	8	US-10-995-561-314 Sequence 314, App
19	36.4	2.1	2941	8	US-10-995-561-315 Sequence 315, App
20	36.4	2.1	3240	12	US-11-052-554A-529 Sequence 529, App

C 21	36.4	2.1	21442	8	US-10-995-561-13469 Sequence 13469, A
C 22	36.4	2.1	35770	12	US-10-995-561-13296 Sequence 13296, A
C 23	36.4	2.1	77246	12	US-11-124-368A-2907 Sequence 2907, App
C 24	36.2	2.1	566	6	US-09-925-065A-732133 Sequence 732133, App
C 25	36	2.1	2745	7	US-10-921-793-73 Sequence 73, Appl
C 26	36	2.1	2745	7	US-10-931-198-73 Sequence 73, Appl
C 27	36	2.1	2745	8	US-10-517-544-76 Sequence 76, Appl
C 28	36	2.1	13884	8	US-10-995-561-13376 Sequence 13376, A
C 29	35.8	2.1	2323	8	US-10-750-185-31877 Sequence 31877, A
C 30	35.8	2.1	2323	8	US-10-750-623-31877 Sequence 31877, A
C 31	35.8	2.1	2552	8	US-10-750-185-55078 Sequence 55078, A
C 32	35.8	2.1	2552	8	US-10-750-623-55078 Sequence 55078, A
C 33	35.8	2.1	3309	9	US-11-072-512-977 Sequence 977, App
C 34	35.8	2.1	6076	12	US-11-136-527-2597 Sequence 2597, App
C 35	35.6	2.1	536	6	US-09-925-065A-535967 Sequence 535967, App
C 36	35.6	2.1	614	6	US-09-925-065A-681562 Sequence 681562, App
C 37	35.6	2.1	138627	7	US-10-330-773-159 Sequence 159, App
C 38	35.4	2.1	1404	8	US-10-750-185-56117 Sequence 56117, A
C 39	35.4	2.1	1404	8	US-10-750-623-56117 Sequence 56117, A
C 40	35.4	2.1	355211	7	US-10-330-773-242 Sequence 242, App
C 41	35.2	2.1	632	6	US-09-925-065A-841922 Sequence 841922, App
C 42	35.2	2.1	1225	8	US-10-750-185-24937 Sequence 24937, A
C 43	35.2	2.1	1225	8	US-10-750-623-24937 Sequence 24937, A
C 44	35.2	2.1	1429	7	US-10-973-115B-485 Sequence 485, App
C 45	35.2	2.1	1429	8	US-10-131-826A-485 Sequence 485, App

ALIGNMENTS

RESULT 1

US-11-072-512-799
; Sequence 799, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAL, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072.512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 799
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-799

Query Match 98.8%; Score 1692.8; DB 9; Length 1785;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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90 ATGCCCGGCCCTGGACACACCCCGCCAGCATCTGGGCCTCCACGCTTGGAGCCGTGGGAG 149
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DB |||||
150 CGGCCAACAGAGCTATGCTCGAGAGCATATGATAAACAACCTCAGCCGCCACCAAGCCGC 209
QY 121 CGCACCCGTAGACACAGACCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCATTAACCTTC 180
DB |||||
210 CGCACCCGTAGACACAGACCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCATTAACCTTC 269
QY 181 ATCTCTGGCTCTGCTCAGCGCGGCCCTTGTAGTCCGCCACCTGTGCTGTCTGGCGACCC 240
DB |||||
270 ATCTCTGGCTCTGCTCAGCGCGGCCCTTGTAGTCCGCCACCTGTGCTGTCTGGCGACCC 329
QY 241 TGGGTGTGGAGTGTGCGCGGCTGCTTCTGTCTCCGCGCTGCGCGGATTCGCTCCAG 300
DB |||||
330 TGGGTGTGGAGTGTGCGCGGCTGCTTCTGTCTCCGCGCTGCGCGGATTCGCTCCAG 389
QY 301 CGCTGTGGAGCTGTGCGGGATGCAGCCCTGCTCTACTCAGAGCTCCACTGAG 360
DB |||||
390 CGCTGTGGAGCTGTGCGGGATGCAGCCCTGCTCTACTCAGAGCTCCACTGAG 449
QY 361 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCAATGAGAGTGCCGCCAGCCCTGATCGT 420
DB |||||
450 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCAATGAGAGTGCCGCCAGCCCTGATCGT 509
QY 421 GCACCCCCCAGCGCGGGATGCGAGCGGCTCAAGTCAACCATGGCGAGCAGCTTCAGC 480
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630 GCCCTGTAGCGGACTCCTGTGCAAGGAGCCACTGGCGGATGCCGCCACCCCAATGCAGAC 689
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690 AGCCTGCCAGCACCTTTGCCAGTAGCTCTCGTGGCTCCGAGGAGTACTTCTTTCCAT 749
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750 GAGTCCGAGCTGAGCTGCGGAGATGGGAGTGGCTCCATGTCGAGCGAGAAATGAT 809
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870 AAGTGCAATCAGACACTGTGTTCTTGGAGAAGACCAAGTAAAGATCTCGACCTTATCAGC 929
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DB |||||
990 ATCATTCGATATGATACCGAAGAGCCGTGCTCGCCCAAGACCTCGAGGGTCTGTCA 1049
QY 961 ACTCGGGCTGCTGCCCAACCGCTGTGCTGCTGACAGTGGCCATGAGACCAATGTTGGGC 1020
DB |||||
1050 ACTCGGGCTGCTGCCCAACCGCTGTGCTGCTGACAGTGGCCATGAGACCAATGTTGGGC 1109
QY 1021 TCAGTCTCAGCCAGGATGAGTGAAGTGCAGATCTCCAGGAGAGAGTGCAGATGCC 1080
DB |||||
1110 TCAGTCTCAGCCAGGATGAGTGAAGTGCAGATCTCCAGGAGAGAGTGCAGATGCC 1169
QY 1081 ATCGCCCGGAAGCTGAGGCTTATGGAGCTCCAGGGTACCAGCAAGCCATGACTCATCC 1140

DB 1170 ATGCCCGGAGCTGAGGCTTATGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC 1229
QY 1141 TTCCAGGGACCGACACAGACTCGTCGGGGGACCCCTTGGCTCCAGGTGTACTGCTAAACC 1200
DB 1230 TTCCAGGGACCGACACAGACTCGTCGGGGGACCCCTTGGCTCCAGGTGTACTGCTAGCC 1289
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DB 1350 GGACCAAGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCACCTCTGGCTCCTCC 1409
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DB 1470 TCTTGTGATCCCGAGCTGTGATCCCTGCGAGGCCCCCTTCTCTCCCTCATGCTCT 1529
QY 1441 TCAGGTGGCTGATCATGGAAGTAGAGAGTTAGGCATTTACCTTCTGGAGTGAAACCTTG 1500
DB 1530 TCAGGTGGCTGATCATGGAAGTAGAGAGTTAGGCATTTACCTTCTGGAGTGAAACCTTG 1589
QY 1501 ACTCCATCCCCCTATTGCCACCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAT 1560
DB 1590 ACTCCATCCCCCTATTGCCACCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAT 1649
QY 1561 TCAACAGTTAAAGAGCTTATCTTAAATGATTTGTTGGGGGTGGGAGGCCCACT 1620
DB 1650 TCAACAGTTAAAGAGCTTATCTTAAATGATTTGTTGGGGGTGGGAGGCCCACT 1709
QY 1621 CTATGTTATGTTAAGGAGTTGTTCTTGGTTCTTGGCTGATGTTCTGTATCTTAAACATGAC 1680
DB 1710 CTATGTTATGTTAAGGAGTTGTTCTTGGTTCTTGGCTGATGTTCTGTATCTTAAACATGAC 1769
QY 1681 CACAGTTTGTAAAGTAC 1696
DB 1770 CACAGTTTGTAAAGTAC 1785

RESULT 2
US-10-501-035-144
; Sequence 144, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 144
; LENGTH: 1738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-501-035-144

Query Match 2.4%; Score 40.6; DB 7; Length 1738;
Best Local Similarity 48.1%; Pred. No. 0.76;
Matches 214; Conservative 0; Mismatches 219; Indels 12; Gaps 3;
QY 2 TGCCCCCGCCCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGAGCCGTGGGAGC 61
DB 188 TGCAGCTGCTGGCCCCCCCCCTTCCCGTGTGGGCTGGACTCCCGGG---GGGTGGC 244

QY 773 AGCTGCCAAGTGCACATCAGACACTGTCTCTGGAGAGACCACTAAGATCTCGGACC 832
Db 473 TGTTTGTGACCCGCAAGGAGTACTTTATCTTCTGGAGTGGCCACGGGGAGGGTGT 532
QY 833 TTATCAGCAGCATCAGCAGGAGTACCACCTCGA 866
Db 533 TTGACTGGATCTGGACCAAGGGCTACTACTCGGA 566

RESULT 6

US-09-925-065A-893863
; Sequence 893863, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 893863
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-893863

Query Match 2.3%; Score 38.6; DB 6; Length 587;

Best Local Similarity 50.3%; Pred. No. 1.9;
Matches 95; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 1081 ATCGCCCGGAAGCTGAGCGCTTATGAGCTCCAGGTTACCCAGCAGCCATGACTCATCC 1140
Db 275 ATGGCATGGAGACGGGGCTGGGGTGGCCAGCGCTCCCGAAGACACTGAGCTACCAAC 334
QY 1141 TTCCAGGGCACCGACACAGACTCGTCGGGGGCACCCCTTGCTCCAGGTGTACTGCTAAACC 1200
Db 335 TTCTACCTCCCTACCACAGCCCTGATCCGATCGCAGCTGCTGTAGTGTGCTAGCGTTCTG 394
QY 1201 CTGCCAGGCCAGCTGCCACACCTTTCTGGGAGAGCATGGCCTTACAGAAATGAAGAGGG 1260
Db 395 CTAGCCTACCAAGTTTGCAACCCCTTGGGTGGAGGAGATAGCGGAGGATGATCCAGGT 454
QY 1261 GCACCAAGGA 1269
Db 455 GCAGGAGGA 463

RESULT 7

US-09-925-065A-894029/c
; Sequence 894029, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 894029
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-894029

Query Match 2.3%; Score 38.6; DB 6; Length 590;

Best Local Similarity 50.3%; Pred. No. 1.9;
Matches 95; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 1081 ATCGCCCGGAAGCTGAGCGCTTATGAGCTCCAGGTTACCCAGCAGCCATGACTCATCC 1140
Db 316 ATGGCATGGAGACGGGGCTGGGGTGGCCAGCGCTCCCGAAGACACTGAGCTACCAAC 257
QY 1141 TTCCAGGGCACCGACACAGACTCGTCGGGGGCACCCCTTGCTCCAGGTGTACTGCTAAACC 1200
Db 256 TTCTACCTCCCTACCACAGCCCTGATCCGATCGCAGCTGCTGTAGTGTGCTAGCGTTCTG 197
QY 1201 CTGCCAGGCCAGCTGCCACACCTTTCTGGGAGAGCATGGCCTTACAGAAATGAAGAGGG 1260
Db 196 CTAGCCTACCAAGTTTGCAACCCCTTGGGTGGAGGAGATAGCGGAGGATGATCCAGGT 137
QY 1261 GCACCAAGGA 1269
Db 136 GCAGGAGGA 128

RESULT 8

US-11-052-554A-519/c
; Sequence 519, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519
; LENGTH: 5706
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-519

Query Match 2.3%; Score 38.6; DB 12; Length 5706;

Best Local Similarity 48.0%; Pred. No. 3.8;
Matches 110; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 103 CAGCCCCCAAGCGCGCACCCGTTAGACCCAGACCCCAAGACCCCTGGCCACCATGGG 162
Db 5107 CGGCCCGCCGATGCGCCTTGCGCGCCCTCACCGCCTTGGCGCGCGCGCCCTCGC 5048
QY 163 CCAGAGAGCATTACCTTCATCTCTGCTGTGAGCCGCCCTTGAGTCCCCACCTGC 222
Db 5047 TCGCCACGCTGTGCTGCTTCCGTTCTGGCGCTCACCCACCGCCCCCGCGGTGCGCGGTGC 4988
QY 223 TGCCTGCTGTGGCGACCCCTTGGGTGTGGAGTGTGTCGGGCTGCCTTCTTCTTCCCGCGC 282

Db 4987 CGCCGGCCCGTTGATGCGCCCGCGCGGTGCGCGCGACCCCGCTTGGCCGCTT 4928
Qy 283 TGCCGGGATTCCTCCAGCGCTGTGGAGCCTGTGTGCGGGGATGACAGCC 331
Db 4927 GCGCGCGCGGAAGCCGTTGCCGTCTTGGAGAGGGCGCGCTGTGCGC 4879

RESULT 9
US-11-136-527-306/c
; Sequence 306, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 306
; LENGTH: 15234
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-306

Query Match 2.2%; Score 37.8; DB 12; Length 15234;
Best Local Similarity 48.8%; Pred. No. 8.6;
Matches 102; Conservative 0; Mismatches 107; Indels 0; Gaps 0;
Qy 162 GCCAGAGAGATACCTTCACTCTGCTCTGCTGAGCGCGCCCTTGAGTCCCGCCACTG 221
Db 5730 GCTGGCCAGAGATACCTTCACTCTGCTGAGCGCGCCCTTGAGTCCCGCCACTG 5671
Qy 222 CTCGCTGCTCTGCGACCCCTGGGTGTGGAGTGGTGGCGGCTGCTTCTGCTTCCGCG 281
Db 5670 GCGCTTCTGTGTGCTGCTGCTGCTGCTGCTGAGCGCGCCAGCTTCTTCTCCAGCAG 5611
Qy 282 CTCGCGGATTCCTCAGCGCTGTGGAGCCTGTGTGCGGGGATGAGCGCCCTGCTGTC 341
Db 5610 CTGCGCGTGTGCTACCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5551
Qy 342 TACTGAGGACTCCACTGAGGGGACTGCTG 370
Db 5550 AGCAGCGCTGTGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5522

RESULT 10
US-11-096-568A-22110/c
; Sequence 22110, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22110
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1431)
; OTHER INFORMATION: Ceres Seq. ID no. 12407603
US-11-096-568A-22110

Query Match 2.2%; Score 37.6; DB 9; Length 1431;

Best Local Similarity 43.3%; Pred. No. 4.7;
Matches 175; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
Qy 11 CTGGACACCCCGCCCGAGCATCTGGGCTTCCACGCTTGGAGCGTGGGAGCGGCCAACAG 70
Db 1182 CTTCTCATCGCTGGCCTTCTTCTTACCTCCCGGAGAGCCTTGCACACAGCATATGC 1123
Qy 71 AGCTATGCTTGGAGACATATGATAACACACCTTCCAGCCCCCAACAGCGCGCGCACCGTA 130
Db 1122 TCTTTTTCACCGTCCGACTCCGACAGCACCTTGGCCATGTGCTGGGCGCGCCGCTGGT 1063
Qy 131 GACACAGACCCCAAGGACCCCTGGCCACCATGGGCGCAGAGAGCATTTACCTTTCATCTCTGGCT 190
Db 1062 GCCATCGTGGCAATCTTCCGCTGCTGCGACCTTGAACCTCCCTCCATGACATGGCGCA 1003
Qy 191 CTGCTGAGCGCGCCCTTGGAGTCCCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 250
Db 1002 CAGCTTTCACGCGCGCCCGGACAGCGCGCTGCTGCGCGGAGCGCGGAGCAGGTGAA 943
Qy 251 AGTGTGCGCGGCTGCTTCTGCTTCCGCGGCTGCGCGGATTCCTCCAGCGCTGTGGAG 310
Db 942 GGTGTGTCAGTGGAACTTGAAGAGCTCTGTTGCGCTGCGGACACACCGAGGGTGTGTTT 883
Qy 311 CCTGTGTGCGGGATGACGCGCCCTGCTGCTTACTGAGGACTCCACTGAGGGGACTGCTG 370
Db 882 CTTGCCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 823
Qy 371 AAGCCAACTGGCGCAGGAGCACAATGAGTGGAGTGGCCCGCCAGCCCT 414
Db 822 CAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779

RESULT 11
US-10-330-773-603
; Sequence 603, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 603
; LENGTH: 38239
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-330-773-603

Query Match 2.2%; Score 37.6; DB 7; Length 38239;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 94; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
Qy 1153 GACACAGACTCTGCGGGGACCCCTTGTCTCCAGGTGTACTGCTAACCCCTGCGAGGCCCA 1212
Db 7967 GCCTGAGGCCCATCGGTAGTGGCTTTACTGCTGATGTAGTGTAGAGAGTGGCTGCTCCC 8026
Qy 1213 GCTGCCACACCCCTTCTGGGAGAGCATGCGCTTACAGATGAAGAGGGGAGCCAGGACC 1272
Db 8027 CTTGCTAGCCCCCTTCCAGGTCAAAGTGGCTCCCAAGAGAGCGGGAGGGGGCAGT 8086
Qy 1273 CTTGCTGGAGAGGCTTAGACCTGAAGCAGTGCCTCTGCTGCTTCTCTCTCTCTGCTGA 1332
Db 8087 CAGTTTGTAGGAGAGACTCAGAAACTTGTGGCTCGGGGCGGTGGACTCAGACTGA 8146
Qy 1333 CTGGGTTC 1340
Db 8147 GTGTTTCC 8154

RESULT 12


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; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 200
; LENGTH: 6034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-501-035-200

Query Match      2.2%; Score 37; DB 7; Length 6034;
Best Local Similarity 50.9%; Pred. No. 11;
Matches 88; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy      330 CCCCTGCTGTCTACTGAGGACTCCACTGAGGGGACTGTGAGCCCACTGGGGCCCAAGGA 389
Db      5868 CCCCGACCCCCCATGAGAGGGGTCACCCCCGGGGGTCCCAAGTTCTGGCTCGCCCAAGGG 5809

Qy      390 GCACAATGAGTGCCTCCAGCCCTGATCGTCACCCCCCAGCCGGCGGATGCCAGCG 449
Db      5808 GTGCACAACTGCCAAGGCACCTCTGCCTGTGTGCGGGGATCCAGGGCAGTGACAGG 5749

Qy      450 GCTCAAGTCAACCATGGGCGAGCAGCTTCACTACCCCGATGTTTAAGCTCAAAG 502
Db      5748 GCCCCAGAGCACGTTGGCAACATGGTGAGGCTGCCCCAGTGTTCAGCGCAAG 5696

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OW nucleic - nucleic search, using sw model

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(without alignments)
11157.652 Million cell updates/sec

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Perfect score: 1713
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Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

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Post-processing: Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1713	100.0	1713	6	AX644347
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5	1197	69.9	1197	6	CQ717675
6	1039	60.7	14207	8	AL356390
7	983	57.4	1977	6	AX535029
8	983	57.4	1977	6	AX535090
9	937	54.7	111738	14	AL592304
10	385	22.5	385	6	AX535028
11	378	22.1	386	6	AX644346
12	334	19.5	393	6	AX069705
13	321	18.7	427	6	AX071660
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15	249	14.5	300	6	BD128735
16	120	7.0	120	6	AX535089
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18	38	2.2	1680	9	BC006890

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20	29	1.7	1718	9	BC079148	BC079148	Rattus no
21	29	1.7	235419	14	AC095979	AC095979	Rattus no
22	29	1.7	249406	14	AC118963	AC118963	Rattus no
23	29	1.7	256017	14	AC126312	AC126312	Rattus no
24	28	1.6	323	6	AX185505	AX185505	Sequence
25	28	1.6	329	6	AX185017	AX185017	Sequence
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27	26	1.5	203	6	AX185663	AX185663	Sequence
28	26	1.5	412	6	AX186486	AX186486	Sequence
29	26	1.5	576	6	CQ424843	CQ424843	Sequence
30	25	1.5	255	6	CQ505617	CQ505617	Sequence
31	25	1.5	275	6	CQ410339	CQ410339	Sequence
32	25	1.5	304	6	CQ475657	CQ475657	Sequence
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35	25	1.5	358	6	CQ421839	CQ421839	Sequence
36	25	1.5	359	6	AX185290	AX185290	Sequence
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41	24	1.4	274	6	CQ398274	CQ398274	Sequence
42	24	1.4	283	6	CQ404561	CQ404561	Sequence
43	24	1.4	283	6	CQ409324	CQ409324	Sequence
44	24	1.4	310	6	CQ396607	CQ396607	Sequence
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46	24	1.4	312	6	CQ397003	CQ397003	Sequence
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53	24	1.4	338	6	AX185287	AX185287	Sequence
54	24	1.4	345	6	CQ476128	CQ476128	Sequence
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62	24	1.4	391	6	CQ402160	CQ402160	Sequence
63	24	1.4	391	6	CQ409304	CQ409304	Sequence
64	24	1.4	392	6	CQ396196	CQ396196	Sequence
65	24	1.4	392	6	CQ402521	CQ402521	Sequence
66	24	1.4	404	6	CQ476176	CQ476176	Sequence
67	24	1.4	409	6	CQ408978	CQ408978	Sequence
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76	24	1.4	426	6	CQ474699	CQ474699	Sequence
77	24	1.4	432	6	CQ411551	CQ411551	Sequence
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79	24	1.4	437	6	CQ396029	CQ396029	Sequence
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82	24	1.4	444	6	CQ408774	CQ408774	Sequence
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85	24	1.4	446	6	CQ504192	CQ504192	Sequence
86	24	1.4	446	6	CQ506124	CQ506124	Sequence
87	24	1.4	446	6	CQ513253	CQ513253	Sequence
88	24	1.4	450	1	KPN293850	KPN293850	Sequence
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C 93	24	1.4	471	6	CQ408780	Sequence	C 166	23	1.3	149	6	CQ475556	Sequence
C 94	24	1.4	486	6	CQ397401	Sequence	C 167	23	1.3	150	6	CQ410075	Sequence
C 95	24	1.4	486	6	CQ403704	Sequence	C 168	23	1.3	150	6	CQ505496	Sequence
C 96	24	1.4	500	6	AX185141	Sequence	C 169	23	1.3	151	6	CQ398966	Sequence
C 97	24	1.4	503	6	CQ409296	Sequence	C 170	23	1.3	151	6	CQ405245	Sequence
C 98	24	1.4	517	6	CQ408905	Sequence	C 171	23	1.3	151	6	AX182151	Sequence
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C 100	24	1.4	521	6	CQ404215	Sequence	C 173	23	1.3	156	6	CQ404236	Sequence
C 101	24	1.4	521	6	CQ408544	Sequence	C 174	23	1.3	157	6	CQ423378	Sequence
C 102	24	1.4	524	6	CQ410821	Sequence	C 175	23	1.3	157	6	CQ506639	Sequence
C 103	24	1.4	524	6	AX185344	Sequence	C 176	23	1.3	160	6	AX182178	Sequence
C 104	24	1.4	529	6	CQ421829	Sequence	C 177	23	1.3	162	6	CQ423447	Sequence
C 105	24	1.4	534	6	CQ398752	Sequence	C 178	23	1.3	167	6	CQ474198	Sequence
C 106	24	1.4	534	6	CQ405034	Sequence	C 179	23	1.3	167	6	CQ505848	Sequence
C 107	24	1.4	546	6	CQ410323	Sequence	C 180	23	1.3	167	6	AX185560	Sequence
C 108	24	1.4	548	6	CQ398971	Sequence	C 181	23	1.3	168	6	CQ397185	Sequence
C 109	24	1.4	548	6	CQ405250	Sequence	C 182	23	1.3	168	6	CQ403489	Sequence
C 110	24	1.4	569	6	CQ507529	Sequence	C 183	23	1.3	168	6	AX185427	Sequence
C 111	24	1.4	569	6	CQ512129	Sequence	C 184	23	1.3	169	6	CQ505687	Sequence
C 112	24	1.4	601	6	CQ411418	Sequence	C 185	23	1.3	170	6	CQ420438	Sequence
C 113	24	1.4	610	6	CQ504182	Sequence	C 186	23	1.3	170	6	CQ475481	Sequence
C 114	24	1.4	610	6	CQ513243	Sequence	C 187	23	1.3	170	6	CQ5066524	Sequence
C 115	24	1.4	610	6	CQ5066129	Sequence	C 188	23	1.3	172	6	CQ399152	Sequence
C 116	24	1.4	619	6	CQ410599	Sequence	C 189	23	1.3	172	6	CQ405430	Sequence
C 117	24	1.4	628	6	CQ410579	Sequence	C 190	23	1.3	172	6	CQ505471	Sequence
C 118	24	1.4	629	6	CQ409923	Sequence	C 191	23	1.3	173	6	CQ5185626	Sequence
C 119	24	1.4	638	6	CQ411867	Sequence	C 192	23	1.3	174	6	CQ475812	Sequence
C 120	24	1.4	646	6	CQ398267	Sequence	C 193	23	1.3	174	6	CQ505525	Sequence
C 121	24	1.4	646	6	CQ404554	Sequence	C 194	23	1.3	176	6	CQ411760	Sequence
C 122	24	1.4	687	6	CQ411193	Sequence	C 195	23	1.3	176	6	CQ475727	Sequence
C 123	24	1.4	739	6	CQ396628	Sequence	C 196	23	1.3	177	6	CQ397399	Sequence
C 124	24	1.4	739	6	CQ402940	Sequence	C 197	23	1.3	177	6	CQ397499	Sequence
C 125	24	1.4	757	6	CQ477202	Sequence	C 198	23	1.3	177	6	CQ403702	Sequence
C 126	24	1.4	818	6	AX554927	Sequence	C 199	23	1.3	177	6	CQ403800	Sequence
C 127	23	1.3	43	6	AX182068	Sequence	C 200	23	1.3	177	6	CQ411609	Sequence
C 128	23	1.3	45	6	AX182081	Sequence	C 201	23	1.3	177	6	CQ504082	Sequence
C 129	23	1.3	54	6	AX182125	Sequence	C 202	23	1.3	177	6	CS067010	Sequence
C 130	23	1.3	60	6	AX182126	Sequence	C 203	23	1.3	177	6	AX185708	Sequence
C 131	23	1.3	79	6	AX182145	Sequence	C 204	23	1.3	178	6	CQ399269	Sequence
C 132	23	1.3	82	6	AX098127	Sequence	C 205	23	1.3	178	6	CQ405547	Sequence
C 133	23	1.3	83	6	AX098165	Sequence	C 206	23	1.3	178	6	CQ476325	Sequence
C 134	23	1.3	85	6	AX182181	Sequence	C 207	23	1.3	179	6	CQ397694	Sequence
C 135	23	1.3	88	6	CQ411855	Sequence	C 208	23	1.3	179	6	CQ403991	Sequence
C 136	23	1.3	92	6	CQ411207	Sequence	C 209	23	1.3	179	6	CS066876	Sequence
C 137	23	1.3	92	6	AX182175	Sequence	C 210	23	1.3	179	6	AX185585	Sequence
C 138	23	1.3	94	6	CS066955	Sequence	C 211	23	1.3	180	6	CQ475482	Sequence
C 139	23	1.3	96	6	CQ411525	Sequence	C 212	23	1.3	181	6	CQ411003	Sequence
C 140	23	1.3	103	6	CQ475988	Sequence	C 213	23	1.3	181	6	CQ506246	Sequence
C 141	23	1.3	111	6	AX182107	Sequence	C 214	23	1.3	183	6	CQ397527	Sequence
C 142	23	1.3	114	6	CQ505443	Sequence	C 215	23	1.3	183	6	CQ403826	Sequence
C 143	23	1.3	116	6	AX098119	Sequence	C 216	23	1.3	184	6	CQ505467	Sequence
C 144	23	1.3	117	6	CS066862	Sequence	C 217	23	1.3	186	6	CQ506288	Sequence
C 145	23	1.3	119	6	AX182110	Sequence	C 218	23	1.3	187	6	CQ476118	Sequence
C 146	23	1.3	120	6	AX098124	Sequence	C 219	23	1.3	187	6	CQ505862	Sequence
C 147	23	1.3	120	6	AX185625	Sequence	C 220	23	1.3	187	6	AX182057	Sequence
C 148	23	1.3	127	6	CQ398993	Sequence	C 221	23	1.3	188	6	CQ398555	Sequence
C 149	23	1.3	127	6	CQ405272	Sequence	C 222	23	1.3	188	6	CQ404842	Sequence
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C 151	23	1.3	128	6	CQ404273	Sequence	C 224	23	1.3	188	6	AX185450	Sequence
C 152	23	1.3	128	6	CQ423639	Sequence	C 225	23	1.3	189	6	CQ409092	Sequence
C 153	23	1.3	133	6	CQ398322	Sequence	C 226	23	1.3	189	6	CQ423425	Sequence
C 154	23	1.3	133	6	CQ404609	Sequence	C 227	23	1.3	190	6	CQ396551	Sequence
C 155	23	1.3	136	6	CQ475585	Sequence	C 228	23	1.3	190	6	CQ402865	Sequence
C 156	23	1.3	140	6	CQ410343	Sequence	C 229	23	1.3	190	6	CQ505834	Sequence
C 157	23	1.3	142	6	CQ397598	Sequence	C 230	23	1.3	191	6	CQ411421	Sequence
C 158	23	1.3	142	6	CQ403897	Sequence	C 231	23	1.3	191	6	CQ475464	Sequence
C 159	23	1.3	142	6	CQ505940	Sequence	C 232	23	1.3	193	6	CQ505767	Sequence
C 160	23	1.3	143	6	CQ411678	Sequence	C 233	23	1.3	194	6	AX185716	Sequence
C 161	23	1.3	147	6	CQ398021	Sequence	C 234	23	1.3	195	6	CQ398734	Sequence
C 162	23	1.3	147	6	CQ404313	Sequence	C 235	23	1.3	195	6	CQ405017	Sequence
C 163	23	1.3	147	6	CS066531	Sequence	C 236	23	1.3	195	6	CQ411656	Sequence
C 164	23	1.3	149	6	CQ398458	Sequence	C 237	23	1.3	195	6	CQ505618	Sequence

C 238	23	1.3	196	6	CQ505054	CQ505054	Sequence	311	23	1.3	250	6	CS066689	CS066689	Sequence
C 239	23	1.3	196	6	CQ506232	CQ506232	Sequence	C 312	23	1.3	251	6	CQ420706	CQ420706	Sequence
C 240	23	1.3	198	6	CQ397731	CQ397731	Sequence	C 313	23	1.3	252	6	CQ506265	CQ506265	Sequence
C 241	23	1.3	198	6	CQ404028	CQ404028	Sequence	C 314	23	1.3	253	6	CQ397814	CQ397814	Sequence
C 242	23	1.3	198	6	AX182091	AX182091	Sequence	C 315	23	1.3	253	6	CQ398199	CQ398199	Sequence
C 243	23	1.3	200	6	CQ399194	CQ399194	Sequence	C 316	23	1.3	253	6	CQ404110	CQ404110	Sequence
C 244	23	1.3	200	6	CQ405472	CQ405472	Sequence	C 317	23	1.3	253	6	CQ404486	CQ404486	Sequence
C 245	23	1.3	200	6	CQ476259	CQ476259	Sequence	C 318	23	1.3	253	6	CQ476305	CQ476305	Sequence
C 246	23	1.3	203	6	CQ398461	CQ398461	Sequence	C 319	23	1.3	254	6	CQ504144	CQ504144	Sequence
C 247	23	1.3	203	6	CQ404748	CQ404748	Sequence	C 320	23	1.3	254	6	AX185509	AX185509	Sequence
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C 249	23	1.3	203	6	CQ411700	CQ411700	Sequence	C 322	23	1.3	255	6	CQ505923	CQ505923	Sequence
C 250	23	1.3	205	6	CQ411178	CQ411178	Sequence	C 323	23	1.3	255	6	AX210928	AX210928	Sequence
C 251	23	1.3	206	6	CQ411356	CQ411356	Sequence	C 324	23	1.3	255	6	AX211025	AX211025	Sequence
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C 253	23	1.3	207	6	AX182113	AX182113	Sequence	C 326	23	1.3	257	6	CQ504093	CQ504093	Sequence
C 254	23	1.3	209	6	CQ396534	CQ396534	Sequence	C 327	23	1.3	257	6	AX185645	AX185645	Sequence
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C 256	23	1.3	209	6	CQ402848	CQ402848	Sequence	C 329	23	1.3	258	6	CQ397646	CQ397646	Sequence
C 257	23	1.3	209	6	CQ405478	CQ405478	Sequence	C 330	23	1.3	258	6	CQ398189	CQ398189	Sequence
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C 262	23	1.3	212	6	CS0666975	CS0666975	Sequence	C 335	23	1.3	259	6	CS0666976	CS0666976	Sequence
C 263	23	1.3	212	6	AX185080	AX185080	Sequence	C 336	23	1.3	260	6	CQ398493	CQ398493	Sequence
C 264	23	1.3	213	6	CQ411410	CQ411410	Sequence	C 337	23	1.3	260	6	CQ404780	CQ404780	Sequence
C 265	23	1.3	214	6	CQ506174	CQ506174	Sequence	C 338	23	1.3	260	6	CQ420734	CQ420734	Sequence
C 266	23	1.3	217	6	CQ475501	CQ475501	Sequence	C 339	23	1.3	260	6	CQ505518	CQ505518	Sequence
C 267	23	1.3	219	6	AX185065	AX185065	Sequence	C 340	23	1.3	261	6	CQ396770	CQ396770	Sequence
C 268	23	1.3	220	6	CQ475461	CQ475461	Sequence	C 341	23	1.3	261	6	CQ403079	CQ403079	Sequence
C 269	23	1.3	221	6	CQ411130	CQ411130	Sequence	C 342	23	1.3	263	6	CQ397565	CQ397565	Sequence
C 270	23	1.3	222	6	CQ410657	CQ410657	Sequence	C 343	23	1.3	263	6	CQ403864	CQ403864	Sequence
C 271	23	1.3	222	6	CQ411279	CQ411279	Sequence	C 344	23	1.3	264	6	CQ398037	CQ398037	Sequence
C 272	23	1.3	224	6	AX185310	AX185310	Sequence	C 345	23	1.3	264	6	CQ398755	CQ398755	Sequence
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C 274	23	1.3	224	6	AX185542	AX185542	Sequence	C 347	23	1.3	264	6	CQ405037	CQ405037	Sequence
C 275	23	1.3	225	6	AX098117	AX098117	Sequence	C 348	23	1.3	264	6	CQ421803	CQ421803	Sequence
C 276	23	1.3	225	6	AX185655	AX185655	Sequence	C 349	23	1.3	265	6	AX098162	AX098162	Sequence
C 277	23	1.3	226	6	CQ398459	CQ398459	Sequence	C 350	23	1.3	266	6	CQ504191	CQ504191	Sequence
C 278	23	1.3	226	6	CQ404746	CQ404746	Sequence	C 351	23	1.3	266	6	CQ513252	CQ513252	Sequence
C 279	23	1.3	227	6	CQ398970	CQ398970	Sequence	C 352	23	1.3	267	6	CQ505829	CQ505829	Sequence
C 280	23	1.3	227	6	CQ405249	CQ405249	Sequence	C 353	23	1.3	267	6	CQ505905	CQ505905	Sequence
C 281	23	1.3	227	6	CQ476120	CQ476120	Sequence	C 354	23	1.3	267	6	AX185140	AX185140	Sequence
C 282	23	1.3	231	6	CQ411021	CQ411021	Sequence	C 355	23	1.3	268	6	CQ398960	CQ398960	Sequence
C 283	23	1.3	234	6	CQ410145	CQ410145	Sequence	C 356	23	1.3	268	6	CQ405239	CQ405239	Sequence
C 284	23	1.3	234	6	CQ505543	CQ505543	Sequence	C 357	23	1.3	268	6	CQ506876	CQ506876	Sequence
C 285	23	1.3	235	6	CQ397693	CQ397693	Sequence	C 358	23	1.3	268	6	AX185496	AX185496	Sequence
C 286	23	1.3	235	6	CQ397814	CQ397814	Sequence	C 359	23	1.3	268	6	AX185659	AX185659	Sequence
C 287	23	1.3	235	6	CQ403990	CQ403990	Sequence	C 360	23	1.3	269	6	CQ423826	CQ423826	Sequence
C 288	23	1.3	235	6	CQ405095	CQ405095	Sequence	C 361	23	1.3	269	6	CQ476142	CQ476142	Sequence
C 289	23	1.3	235	6	CQ421976	CQ421976	Sequence	C 362	23	1.3	269	6	AX185675	AX185675	Sequence
C 290	23	1.3	235	6	CQ475692	CQ475692	Sequence	C 363	23	1.3	271	6	CQ397883	CQ397883	Sequence
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C 292	23	1.3	237	6	CQ475658	CQ475658	Sequence	C 365	23	1.3	271	6	CQ409873	CQ409873	Sequence
C 293	23	1.3	238	6	AX182139	AX182139	Sequence	C 366	23	1.3	271	6	CQ423798	CQ423798	Sequence
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C 296	23	1.3	241	6	CQ476374	CQ476374	Sequence	C 369	23	1.3	272	6	CQ398306	CQ398306	Sequence
C 297	23	1.3	241	6	CS0666238	CS0666238	Sequence	C 370	23	1.3	272	6	CQ404373	CQ404373	Sequence
C 298	23	1.3	244	6	CQ475970	CQ475970	Sequence	C 371	23	1.3	272	6	CQ404593	CQ404593	Sequence
C 299	23	1.3	246	6	CQ398352	CQ398352	Sequence	C 372	23	1.3	273	6	CQ398161	CQ398161	Sequence
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C 301	23	1.3	246	6	AX185506	AX185506	Sequence	C 374	23	1.3	276	6	AX182105	AX182105	Sequence
C 302	23	1.3	247	6	CQ411583	CQ411583	Sequence	C 375	23	1.3	277	6	CQ505765	CQ505765	Sequence
C 303	23	1.3	247	6	CS0666733	CS0666733	Sequence	C 376	23	1.3	277	6	CQ506088	CQ506088	Sequence
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C 385	23	1.3	282	6	CQ403941	Sequence	C 458	23	1.3	309	6	CQ398530	Sequence
C 386	23	1.3	282	6	CQ404924	Sequence	C 459	23	1.3	309	6	CQ402406	Sequence
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C 390	23	1.3	283	6	CQ401352	Sequence	C 463	23	1.3	310	6	AX098104	Sequence
C 391	23	1.3	283	6	CQ410861	Sequence	C 464	23	1.3	310	6	AX182117	Sequence
C 392	23	1.3	285	6	CQ505426	Sequence	C 465	23	1.3	311	6	CS066060	Sequence
C 393	23	1.3	285	6	CS066841	Sequence	C 466	23	1.3	312	6	CQ422033	Sequence
C 394	23	1.3	287	6	CQ398527	Sequence	C 467	23	1.3	312	6	AX185485	Sequence
C 395	23	1.3	287	6	CQ399239	Sequence	C 468	23	1.3	313	6	CQ399000	Sequence
C 396	23	1.3	287	6	CQ404814	Sequence	C 469	23	1.3	313	6	CQ405279	Sequence
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C 404	23	1.3	289	6	CQ410178	Sequence	C 477	23	1.3	315	6	CQ420840	Sequence
C 405	23	1.3	289	6	CS066248	Sequence	C 478	23	1.3	315	6	AX185063	Sequence
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C 407	23	1.3	290	6	CQ474853	Sequence	C 480	23	1.3	316	6	CQ410443	Sequence
C 408	23	1.3	291	6	CQ506025	Sequence	C 481	23	1.3	317	6	CQ395989	Sequence
C 409	23	1.3	292	6	CQ475950	Sequence	C 482	23	1.3	317	6	CQ398516	Sequence
C 410	23	1.3	293	6	CQ397716	Sequence	C 483	23	1.3	317	6	CQ402317	Sequence
C 411	23	1.3	293	6	CQ404013	Sequence	C 484	23	1.3	317	6	CQ404803	Sequence
C 412	23	1.3	295	6	CQ398598	Sequence	C 485	23	1.3	317	6	CQ423788	Sequence
C 413	23	1.3	295	6	CQ404883	Sequence	C 486	23	1.3	317	6	AX182115	Sequence
C 414	23	1.3	295	6	AX182183	Sequence	C 487	23	1.3	318	6	CQ397463	Sequence
C 415	23	1.3	296	6	CQ397404	Sequence	C 488	23	1.3	318	6	CQ397569	Sequence
C 416	23	1.3	296	6	CQ398869	Sequence	C 489	23	1.3	318	6	CQ403764	Sequence
C 417	23	1.3	296	6	CQ403707	Sequence	C 490	23	1.3	318	6	CQ403868	Sequence
C 418	23	1.3	296	6	CQ405149	Sequence	C 491	23	1.3	318	6	CQ475564	Sequence
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C 422	23	1.3	297	6	CQ424781	Sequence	C 495	23	1.3	321	6	CQ403078	Sequence
C 423	23	1.3	298	6	CQ395946	Sequence	C 496	23	1.3	321	6	CQ474928	Sequence
C 424	23	1.3	298	6	CQ402274	Sequence	C 497	23	1.3	321	6	CQ505561	Sequence
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AX644347

LOCUS

AX644347

SEQUENCE 105 from Patent WO02077232.

DEFINITION

AX644347

ACCESSION

AX644347.1

VERSION

GI:28610406

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

Salceda,S., Macina,R.A., Recipon,H., Pluta,J., Sun,Y. and Liu,C. Compositions and methods relating to breast specific genes and proteins

JOURNAL

Patent: WO 02077232-A 105 03-OCT-2002;

Diadexus, Inc. (US)

FEATURES

Location/Qualifiers

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ALIGNMENTS

linear PAT 27-FEB-2003

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,B.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1679)
.
NIH MGC Project
Direct Submission
Submitted (25-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca

Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
Wong, Corey Matasu, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim Macdonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR
Santos, Duane Smailus, Jeff Scott, Miranda Tsai, George Yang,
Jacquie Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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Location/Qualifiers

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ACCESSION AX747274
VERSION AX747274.1 GI:32131662
KEYWORDS
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.
Full-length cDNA sequences
Patent: EP 1308459-A 799 07-MAY-2003;
Helix Research Institute (JP); Research Association for
Biotechnology (JP)
FEATURES
Location/Qualifiers
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Best Local Similarity 99.9%; Pred. No. 0;
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VERSION	AK091952.1	GI:21750433	
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ORGANISM	Homo sapiens		
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AUTHORS			
1	Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamiyama, K., Ishibashi, T., Yamashita, H., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Kanehori, S., Tanabe, M., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Mueshino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshihara, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiya, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y.,		

Osaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.			
Complete sequencing and characterization of 21,243 full-length human cDNAs			
Nat. Genet. 36 (1), 40-45 (2004)			
14702039			
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Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.			
NEDO human cDNA sequencing project			
Unpublished			
3 (bases 1 to 1785)			
Isogai, T. and Yamamoto, J.			
Direct Submission			
Submitted (04-JUL-2002)			
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan			
(E-mail: genomics@kri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)			
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.			
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ORIGIN			
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Best Local Similarity			
Matches 1694; Conservative			
93.1%; Score 1594; DB 8; Length 1785;			
99.9%; Pred. No. 0;			
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2; Indels			
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Qy	61	CGGCCACACAGAGCTATGTCTGGAGACATATGATATAAACACCACTCAGGCCCCACCAAGCGC	120
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Qy	181	ATCTCTGGCTCTGCTGAGCGCGCCCTTGAGTCCCCACCTGCTGCTGCTGCTGCGGCC	240
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Qy	241	TGGGTGTGGGAGTGGTGC CGGGCTGCTTCTGCTTCCGCGCTGCGGGATTGCTCCAG	300
Db	82259	TGGGTGTGGGAGTGGTGC CGGGCTGCTTCTGCTTCCGCGCTGCGGGATTGCTCCAG	82358
Qy	301	CGCTGTGAGCCTGTGTGCGGGATGACGCCCCCTGCTGCTTACTGAGGACTCCACTGAG	360
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Qy	361	GGGACTGCTGAAGCAACTGGGCCCAAGGAGCACAAATGGAGTCCCGCCAGCCCTGATCGT	420
Db	82419	GGGACTGCTGAAGCAACTGGGCCCAAGGAGCACAAATGGAGTCCCGCCAGCCCTGATCGT	82478
Qy	421	GCACCCCCCAGCGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGAGCAGCTTCAGC	480
Db	82479	GCACCCCCCAGCGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGAGCAGCTTCAGC	82538
Qy	481	TACCCCGATGTTAAGCTCAAGGCAATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCA	540
Db	82539	TACCCCGATGTTAAGCTCAAGGCAATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCA	82598
Qy	541	GCCCTGTATGCGGACTCCTGCTGCAAGGAGCACTTGGCCGATCCCCACCCATCGCAC	600
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Qy	601	AGCCTGCCAGCACCTTTGCCAGTAGTCTCTGCTGGCTCCGAGGAGTACTATTTTCCAT	660
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Db	82719	GAGTCGACCTGAGACTTGC CGGAGATGGGAGTGGCTTCCATGTGAGCCGAGAAATTGAT	82778
Qy	721	GTGCTCATCTTCAAGAGCTCACAGAGCTTTCAGCGTACACCATGATGAGTGGCGC	780
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Qy	1021	TCAGGTCTCAGCCAGGATG 1039	
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DEFINITION Sequence 56 from Patent WO02068633.
ACCESSION AX535029
VERSION AX535029.1 GI:25261664
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.
1
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN
Query Match 57.48; Score 983; DB 6; Length 1977;
Best Local Similarity 99.99; Pred. No. 0;
Matches 1103; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
Compositions and methods relating to lung specific genes and
proteins
Patent: WO 02068633-A 56 SEP-2002;
Diadexus, Inc. (US)
Location/Qualifiers
1. .1977
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Qy	658	CATGAGTCGACCTGCGACCTGTCGCGAGATGGGCACTGCTCCATGTGAGCCGAGAAATT	717
Db	921	CATGAGTCGACCTGCGACCTGTCGCGAGATGGGCACTGCTCCATGTGAGCCGAGAAATT	980
Qy	718	GATGTGCTCATCTTCAAGAGCTGACAGAGCTGTTTCCAGCGTACACCATGATGAGCT	776
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Qy	777	GGCCAAATGTCACATCAGACACTGTGTTCTCGGAGAGACCAAGTAAAGTCTCGGACCTTAT	836
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Qy	837	CAGCAGCATACGCGAGCTACACCTTGATGAGCAGATGCTGAGGGCCGCTTGGTACG	896
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Qy	897	CGGCATCTTCGANTAGTACCGAAGAGCGGTGCTGCCCCACAGACCTCGGAGGGTCG	956
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Db	1221	TTCAACTCGGGCTGCTGCCCCCAACCGCTGCTGCCCTTGACAGTGGCCATGAGACCATGGT	1280
Qy	1017	GGGCTCAGGTCTCAGCAGGATGAGCTGACAGTGCAGATCTCCAGAGAGCAGCTGCAGA	1076
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Qy	1077	TGCCATCGCCGGAAGCTGAGGGCTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTC	1136
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Qy	1137	ATCCTTCCAGGGCACCGACACAGACTCGTCCGGGGCACCCCTTGCTCCAGGTGTACTGCTA	1196
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Qy	1197	ACCCCTGCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGGCTACAGAAATGAG	1256
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COMMENT

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----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dj426N7
----- Summary Statistics
Sequencing program: XGAP4; version 4.5
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 110287 bases at least Q40
Consensus quality: 110500 bases at least Q30
Consensus quality: 110681 bases at least Q20
Insert size: 111138; sum-of-contigs
Insert size: 119403; 8.4% error; agarose-fp
Quality coverage: 11.21x in Q20 bases; sum-of-contigs Quality
coverage: 10.67x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 18058: contig of 18058 bp in length
* 18059 18158: gap of 100 bp
* 18159 35144: contig of 16986 bp in length
* 35145 35244: gap of 100 bp
* 35245 54710: contig of 19466 bp in length
* 54711 54810: gap of 100 bp
* 54811 72936: contig of 18126 bp in length
* 72937 73036: gap of 100 bp
* 73037 92888: contig of 19852 bp in length
* 92889 108739: contig of 15751 bp in length
* 108740 108839: gap of 100 bp
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Qy 61 CGGCCAACAGAGCTATGCTGGAGACATATGATAAACAACCTCAGCCGCCACCAAGCCGC 120
Db 95786 CGGCCAACAGAGCTATGCTGGAGACATATGATAAACAACCTCAGCCGCCACCAAGCCGC 95845

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Qy 301 CGCTGTGAGCGCTGTGTGCGGGGATGACGCCCCCTGCTGCTTACTGAGGACTCCACTGAG 360
Db 96026 CGCTGTGAGCGCTGTGTGCGGGGATGACGCCCCCTGCTGCTTACTGAGGATTCCACTGAG 96085

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Db 96086 GGGACTCTGTAAGCCAACTGGGCCAAGGAGACAAATGGAGTGGCCCCCAGCCCTGATCGT 96145

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Db 96506 AAGTGACATCAGACACTGTGTTCTCGAGAGACCAAGTAAAGATCTCGGACCTTATCAGC 96565

Qy 841 AGCATACGCGAGGACTACCACTGGATGAGCAGATGCTGAGGGCCGCTGGTACGCGGC 900
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Qy 961 ACTCGGCTGCTGCCCAACCGCTGTGCCCTGACGATGGCCATGAGCCATGGTGGC 1020
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DEFINITION AX535028
ACCESSION AX535028
VERSION AX535028.1 GI:25261662
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
TITLE Compositions and methods relating to lung specific genes and
proteins
JOURNAL Patent: WO 02068633-A 55 06-SEP-2002;
Diadexus, Inc. (US)
FEATURES
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AX644346 AX644346 386 bp DNA linear PAT 27-FEB-2003
LOCUS Sequence 104 from Patent WO02077232.
DEFINITION AX644346
ACCESSION AX644346
VERSION AX644346.1 GI:28610405
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.,
Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.,
Lamson, G., Dmanac, R., Crkenjakov, R., Drmanac, S., Dickson, M.,
Labat, I., Leshkowitz, D., Kita, D., Garcia, V. and Strache-Crain, B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0102568-A 177 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Salceda, S., Macina, R.A., Recipon, H., Pluta, J., Sun, Y. and Liu, C.
TITLE Compositions and methods relating to breast specific genes and
proteins
JOURNAL Patent: WO 02077232-A 104 03-OCT-2002;
Diadexus, Inc. (US)
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Db 69 ACCAGGAACCCCTGTGGAGAGGCTTAGACCTGAAGCAGTGCCTCTGGCTCTCTCTG 128
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Qy 1563 AACAGTTAAAGAGCTT 1580
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Db 369 AACAGTTAAAGAGCTT 386
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LOCUS Sequence 177 from Patent WO0102568.
DEFINITION AX069705
ACCESSION AX069705
VERSION AX069705.1 GI:12579490
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.,
Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.,
Lamson, G., Dmanac, R., Crkenjakov, R., Drmanac, S., Dickson, M.,
Labat, I., Leshkowitz, D., Kita, D., Garcia, V. and Strache-Crain, B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0102568-A 177 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.6e-09;
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RESULT 19
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LOCUS Mouse DNA sequence from clone RP23-137L22 on chromosome 4, complete
DEFINITION sequence.

ACCESSION
VERSION AL627228.31 GI:28208155
KEYWORDS HTG.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 193813)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (04-FEB-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 4, 2003 this sequence version replaced gi:22474404.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was finished as follows unless otherwise noted: all regions were
either double-stranded or sequenced with an alternate chemistry or
covered by high quality data (i.e., phred quality >= 30); an
attempt was made to resolve all sequencing problems, such as
compressions and repeats; all regions were covered by at least one
plasmid subclone or more than one M13 subclone; and the assembly
was confirmed by restriction digest, except on the rare occasion of
the clone being a YAC.

RP23-137L22 is from the RPCI-23 Mouse BAC Library

constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBAC3.6

Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.

FEATURES

source

1..193813
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="4"
/clone="RP23-137L22"
/clone_lib="RPCI-23"

ORIGIN

Query Match

2.2%; Score 38; DB 9; Length 193813;

Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCACGAGGACTACCACTGGATGAGCA 872
|||||
DB 104723 ATCAGCAGCATCACGAGGACTACCACTGGATGAGCA 104760
|||||

RESULT 20

BC079148

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 1718)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Howard Jacobs

cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcdepaxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAX Plate: 184 Row: d Column: 16

This clone was selected for full length sequencing because it

passed the following selection criteria: Hexamer frequency ORF

analysis, similarity but not identity to protein.

Location/Qualifiers

1..1718

/organism="Rattus norvegicus"

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/lab_host="DH10B"
/notes="Vector: pExpress1"
1. 1718
/gene="MGC94165"
/db_xref="GeneID:313018"
73. 1266
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/codon_start=1
/product="similar to hypothetical protein FLJ34633"
/db_xref="GI:50927713"
/db_xref="GeneID:313018"
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YDVKLAGIPVYVRHATSPVPDADSCKEPLADPPTRHSLPSTPTSSPRGSEYVS
FHESDLIPWSSGMSREIDVLI PKLTELFSVHQLDELAKTSTVTFLEKTSKLS
DLISITQDYLHLDQDAEGLVRLGIIIRIKTRKSRSPQTSEGRARSATPAAPDSGH
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LQVYC"

ORIGIN
Query Match 1.7%; Score 29; DB 9; Length 1718;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 994 GACAGTGCCCATGAGACCATGGTGGGCTC 1022
|||||
Db 1063 GACAGTGCCCATGAGACCATGGTGGGCTC 1091
|||||

RESULT 21
AC095979 235419 bp DNA linear HTG 09-NOV-2002
LOCUS Rattus norvegicus clone CH230-11020, WORKING DRAFT SEQUENCE, 3
DEFINITION Unordered pieces.
ACCESSION AC095979
VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Rattus.
1 (bases 1 to 235419)
Muzny,D,Marie, Metzker,M, Lee, Abramzon,S, Adams,C, Alder,J,
Allen,C, Allen,H, Albrooks,S, Amin,A, Anguiano,D,
Anyalebechi,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H,
Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F,
Biswalo,K, Blair,J, Blankenburg,K, Blyth,P, Brown,M,
Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E,
Cardenas,V, Carter,K, Cavazos,I, Ceasar,H, Chen,A,
Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
Davila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D,
Delgado,O, Denson,S, Deramo,C, Ding,Y, Dinh,H, Divya,K,
Draper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Eaves,K,
Egan,A, Escotto,M, Eugene,C, Evans,C, Falls,T, Fan,G,
Fernandez,S, Finley,M, Flaggs,N, Forbes,L, Foster,M, Foster,P,
Fraser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M,
Gebregiorgis,E, Geer,K, Gill,R, Grady,M, Guerra,M, Guevara,W,
Gunaratne,P, Haaland,W, Hamill,C, Hamilton,C, Hamilton,K,
Harvey,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,J,
Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M,
Hollins,B, Howells,S, Hulyk,S, Hume,J, Idlebird,D, Jackson,A,
Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolivet,A,
Karpathy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovar,C,
Kowitz,C, Kraft,C,L, Lebow,H, Levan,J, Lewis,L, Li,Z, Liu,J,
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Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheehwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,D.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokemelele,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.,
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Taber,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villaseana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 235419)
Worley,K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235419)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:22772470.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GEBU
Center clone name: CH230-11020
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 225536 bases at least Q40
Consensus quality: 227458 bases at least Q30
Consensus quality: 228649 bases at least Q20
Estimated insert size: 235033; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
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* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 221492: contig of 221492 bp in length
* 221493: gap of unknown length
* 221593: contig of 7059 bp in length
* 228651: contig of 7059 bp in length
* 228652: gap of unknown length
* 228751: gap of unknown length
* 228752: contig of 6668 bp in length.
* 228753: Location/Qualifiers
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        219511..220573
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            end_sequence:BH344813"
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    Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 994 GACATGCGCATGAGACCATGCTGGGCTC 1022
Db 84076 GACATGCGCATGAGACCATGCTGGGCTC 84104
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AC118963/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
1 (bases 1 to 249406)
Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allien,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Dirig,Y., Dinh,H., Divya,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregorgis,E., Gear,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,M., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,

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Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorenshewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartine,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwackeleme,O., Okwuonu,G., Olarunpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfamkotch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
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Sanders,W., Savery,G., Scherer,S., Scott,G., Shatman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
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Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 249406)
Worley,K.C.
Direct Submission
Submitted (22-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 249406)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23269749.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GVHY
Center clone name: CH230-18084
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 213357 bases at least Q40
Consensus quality: 215358 bases at least Q30
Consensus quality: 217213 bases at least Q20
Estimated insert size: 223109; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

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* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 249406: contig of 249406 bp in length.
FEATURES
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ORIGIN
Query Match 1.7%: Score 29; DB 14; Length 249406;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 994 GACAGTGCCCATGAGACCATGGTGGCTC 1022
 |||||
DB 13766 GACAGTGCCCATGAGACCATGGTGGCTC 13738

RESULT 23
AC126312/c
LOCUS
DEFINITION Rattus norvegicus clone CH230-1B9, *** SEQUENCING IN PROGRESS ***,
3 unordered pieces.
AC126312
AC126312.4 GI:24941465
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Rattus.
1 (bases 1 to 256017)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brivea,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
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Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Kratovich,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulsged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,G., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtonson,J., Newtonson,N., Nguyen,A., Nguyen,N.,

Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickets,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaika,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Thomas,S.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Wang,Q.,
Umani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
2 (bases 1 to 256017)
Worley,K.C.
Direct Submission
Submitted (05-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 256017)
Worley,K.C.
Direct Submission
Submitted (13-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:23267435.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: RUNJ
Center clone name: CH230-1B9
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 214827 bases at least Q40
Consensus quality: 219116 bases at least Q30
Consensus quality: 221911 bases at least Q20
Estimated insert size: 222841; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 83721: contig of 83721 bp in length
* 83722 83821: gap of unknown length
* 83822 253567: contig of 169746 bp in length
* 253568 253667: gap of unknown length
* 253668 256017: contig of 2350 bp in length.
FEATURES
 Location/Qualifiers
 1..256017
source


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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-1B9"
6668..7475
/note="clone_boundary
clone_end:17"
site:
end_sequence:BH274997"
38358..39527
/note="wgs_contig"
67950..69005
/note="wgs_contig"
78781..81213
/note="wgs_contig"
83722..83821
/estimated_length=unknown
83822..85574
/note="wgs_contig"
219978..221353
/note="wgs_contig"
253568..253667
/estimated_length=unknown

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 994 GACAGTGCCATGACGACCATGGTGGCTC 1022
Db 154754 GACAGTGCCATGACGACCATGGTGGCTC 154726

RESULT 24
AX185505/c AX185505 323 bp DNA linear PAT 06-AUG-2001
LOCUS
DEFINITION Sequence 1200 from Patent WO0142467.
ACCESSION AX185505
VERSION AX185505.1 GI:15136902
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Schlegel,R., Deeds,J., Berger,A. and Zhao,X.
AUTHORS Genes, compositions, kits, and methods for identification,
TITLE assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 1200 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source
Location/Qualifiers
1..323
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.6%; Score 28; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1686 TTGTAGTACCTCGCGCGACCAACGC 1713
Db 34 TTGTAGTACCTCGCGCGACCAACGC 7

RESULT 25
AX185017/c AX185017 329 bp DNA linear PAT 06-AUG-2001
LOCUS
DEFINITION Sequence 712 from Patent WO0142467.
ACCESSION AX185017
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VERSION AX185017.1 GI:15136393
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Schlegel,R., Deeds,J., Berger,A. and Zhao,X.
AUTHORS Genes, compositions, kits, and methods for identification,
TITLE assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 712 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source
Location/Qualifiers
1..329
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.6%; Score 28; DB 6; Length 329;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1686 TTGTAGTACCTCGCGCGACCAACGC 1713
Db 34 TTGTAGTACCTCGCGCGACCAACGC 7

RESULT 26
AX098107/c AX098107 91 bp DNA linear PAT 30-MAR-2001
LOCUS
DEFINITION Sequence 19 from Patent WO0118542.
ACCESSION AX098107
VERSION AX098107.1 GI:13514986
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Lee,J., Thompsho,P. and Lillie,J.
AUTHORS Identification, assessment, prevention, and therapy of ovarian
TITLE cancer
JOURNAL Patent: WO 0118542-A 19 15-MAR-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source
Location/Qualifiers
1..91
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAAGTACCTCGCGCGACCAACGC 1713
Db 32 TGTAAGTACCTCGCGCGACCAACGC 7

RESULT 27
AX185663/c AX185663 203 bp DNA linear PAT 06-AUG-2001
LOCUS
DEFINITION Sequence 1358 from Patent WO0142467.
ACCESSION AX185663
VERSION AX185663.1 GI:15137068
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
1 Hominidae; Homo.
REFERENCE
AUTHORS Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
TITLE Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 1358 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source Location/Qualifiers
1..203
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1688 TGTAAGTACCTCGCGCGACACGC 1713
Db 32 TGTAAGTACCTCGCGCGACACGC 7
RESULT 28
AX186486
LOCUS AX186486 412 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 2181 from Patent WO0142467.
ACCESSION AX186486
VERSION AX186486.1 GI:15137921
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
TITLE Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 2181 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 412;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1686 TTTGTAAGTACCTCGCGCGACAC 1711
Db 377 TTTGTAAGTACCTCGCGCGACAC 402
RESULT 29
CQ424843
LOCUS CQ424843 576 bp DNA linear PAT 28-JAN-2004
DEFINITION Sequence 9877 from Patent WO0151628.
ACCESSION CQ424843
VERSION CQ424843.1 GI:41377072
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
TITLE Novel genes, compositions, kits, and methods for identification,

assessment, prevention, and therapy of breast cancer
Patent: WO 0151628-A 9877 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1..576
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 576;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1688 TGTAAGTACCTCGCGCGACACGC 1713
Db 550 TGTAAGTACCTCGCGCGACACGC 575
RESULT 30
CQ505617/c
LOCUS CQ505617 255 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 37484 from Patent WO0160860.
ACCESSION CQ505617
VERSION CQ505617.1 GI:41471716
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 37484 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source Location/Qualifiers
1..255
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.5%; Score 25; DB 6; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1689 GTAAGTACCTCGCGCGACACGC 1713
Db 97 GTAAGTACCTCGCGCGACACGC 73
RESULT 31
CQ410339/c
LOCUS CQ410339 275 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 17410 from Patent WO0170979.
ACCESSION CQ410339
VERSION CQ410339.1 GI:41318120
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 17410 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match      1.5%; Score 25; DB 6; Length 275;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAAGTACCTCGCGCGGACCAACGC 1713
Db 87 GTAAGTACCTCGCGCGGACCAACGC 63

RESULT 32
LOCUS      CQ475657          304 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 7524 from Patent WO0160860.
ACCESSION  CQ475657
VERSION     CQ475657.1 GI:41441276
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Schlegel, R., Endege, W.O. and Monahan, J.R.
TITLE       Genes differentially expressed in human prostate cancer and their
JOURNAL     use
FEATURES    source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN

Query Match      1.5%; Score 25; DB 6; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAAGTACCTCGCGCGGACCAACGC 1713
Db 39 GTAAGTACCTCGCGCGGACCAACGC 15

RESULT 33
LOCUS      CQ398024          310 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 5095 from Patent WO0170979.
ACCESSION  CQ398024
VERSION     CQ398024.1 GI:41305805
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Lee, J. and Lillie, J.
TITLE       Genes, compositions, kits, and method for identification,
JOURNAL     assessment, prevention, and therapy of ovarian cancer
FEATURES    source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN

Query Match      1.5%; Score 25; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAAGTACCTCGCGCGGACCAACGC 1713
Db 280 GTAAGTACCTCGCGCGGACCAACGC 304

RESULT 34
LOCUS      CQ404316          310 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 11387 from Patent WO0170979.
ACCESSION  CQ404316
VERSION     CQ404316.1 GI:41312097
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Lee, J. and Lillie, J.
TITLE       Genes, compositions, kits, and method for identification,
JOURNAL     assessment, prevention, and therapy of ovarian cancer
FEATURES    source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN

Query Match      1.5%; Score 25; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAAGTACCTCGCGCGGACCAACGC 1713
Db 280 GTAAGTACCTCGCGCGGACCAACGC 304

RESULT 35
LOCUS      CQ421839          358 bp DNA linear PAT 28-JAN-2004
DEFINITION Sequence 6873 from Patent WO0151628.
ACCESSION  CQ421839
VERSION     CQ421839.1 GI:41374068
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
TITLE       Novel genes, compositions, kits, and methods for identification,
JOURNAL     assessment, prevention, and therapy of breast cancer
FEATURES    source
            1..358
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN

Query Match      1.5%; Score 25; DB 6; Length 358;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAAGTACCTCGCGCGGACCAACGC 1713
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Db 31 GTAAGTACCTCGCGCGGACACGC 7
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AX185290 359 bp DNA linear PAT 06-AUG-2001
LOCUS Sequence 985 from Patent WO0142467.
ACCESSION AX185290
VERSION AX185290.1 GI:15136678
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
TITLE Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 985 14-JUN-2001;
Mileennium Predictive Medicine, Inc. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 1.5%; Score 25; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1689 GTAAGTACCTCGCGCGGACACGC 1713
|||||
Db 31 GTAAGTACCTCGCGCGGACACGC 7
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RESULT 37
CQ410700 463 bp DNA linear PAT 23-JAN-2004
LOCUS Sequence 17771 from Patent WO0170979.
DEFINITION CQ410700
ACCESSION CQ410700
VERSION CQ410700.1 GI:41318481
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 17771 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source 1. .463
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 1.5%; Score 25; DB 6; Length 463;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1689 GTAAGTACCTCGCGCGGACACGC 1713
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Db 351 GTAAGTACCTCGCGCGGACACGC 375
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RESULT 38

CS067068/c 150 bp DNA linear PAT 20-APR-2005
LOCUS Sequence 1051 from Patent WO2005030998.
ACCESSION CS067068
VERSION CS067068.1 GI:62819876
KEYWORDS
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1
REFERENCE
AUTHORS Berka, R., Bashkirova, E. and Rey, M.
TITLE Methods for monitoring multiple gene expression
JOURNAL Patent: WO 2005030998-A 1051 07-APR-2005;
Novozymes Biotech, Inc. (US)
FEATURES
source 1. .150
/organism="Hypocrea jecorina"
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/db_xref="taxon:51453"
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Query Match 1.4%; Score 24; DB 6; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACCTCGCGCGGACACGC 1713
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Db 24 TAAGTACCTCGCGCGGACACGC 1
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RESULT 39
AX718965 232 bp DNA linear PAT 15-APR-2003
LOCUS Sequence 15 from Patent WO03002599.
DEFINITION AX718965
ACCESSION AX718965
VERSION AX718965.1 GI:29891501
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS Encinas, J. and Leong, J.
TITLE Immune-related proteins and the regulation of the same
JOURNAL Patent: WO 03002599-A 15 09-JAN-2003;
Bayer Aktiengesellschaft (DE)
FEATURES
source 1. .232
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Query Match 1.4%; Score 24; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1688 TGTAAGTACCTCGCGCGGACACGC 1711
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Db 207 TGTAAGTACCTCGCGCGGACACGC 230
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RESULT 40
CQ410151/c 253 bp DNA linear PAT 23-JAN-2004
LOCUS Sequence 17222 from Patent WO0170979.
DEFINITION CQ410151
ACCESSION CQ410151
VERSION CQ410151.1 GI:41317932
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1
Lee, J. and Lillie, J.
Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 1722 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers

1. .253
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 1.4%; Score 24; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
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Db 77 TAAGTACTCGCGCGACACGC 54
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RESULT 41
CQ398274/c
LOCUS CQ398274 274 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 5345 from Patent WO0170979.
ACCESSION CQ398274
VERSION CQ398274.1 GI:41306055
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1
Lee, J. and Lillie, J.
Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 5345 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers

1. .274
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 1.4%; Score 24; DB 6; Length 274;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
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Db 30 TAAGTACTCGCGCGACACGC 7
|||||

RESULT 42
CQ404561/c
LOCUS CQ404561 274 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 11632 from Patent WO0170979.
ACCESSION CQ404561
VERSION CQ404561.1 GI:41312342
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1
Lee, J. and Lillie, J.

Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 11632 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers

1. .274
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 1.4%; Score 24; DB 6; Length 274;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACTCGCGCGACACGC 7
|||||

RESULT 43
CQ409324/c
LOCUS CQ409324 283 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 16395 from Patent WO0170979.
ACCESSION CQ409324
VERSION CQ409324.1 GI:41317105
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1
Lee, J. and Lillie, J.
Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 16395 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers

1. .283
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 1.4%; Score 24; DB 6; Length 283;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
|||||
Db 54 TAAGTACTCGCGCGACACGC 31
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RESULT 44
CQ396607/c
LOCUS CQ396607 310 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 3678 from Patent WO0170979.
ACCESSION CQ396607
VERSION CQ396607.1 GI:41304388
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1
Lee, J. and Lillie, J.
Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 3678 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers

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source
1. .310
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 24; DB 6; Length 310;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1690 TAAGTACTCGCGCGGACACGC 1713
Db 30 TAAGTACTCGCGCGGACACGC 7

RESULT 45
LOCUS CQ402920/c 310 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 9991 from Patent WO0170979.
ACCESSION CQ402920
VERSION CQ402920.1 GI:41310701
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 991 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
1. .310
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 24; DB 6; Length 310;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1690 TAAGTACTCGCGCGGACACGC 1713
Db 30 TAAGTACTCGCGCGGACACGC 7

RESULT 46
LOCUS CQ397003/c 312 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 4074 from Patent WO0170979.
ACCESSION CQ397003
VERSION CQ397003.1 GI:41304784
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 4074 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
1. .312
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 24; DB 6; Length 312;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1690 TAAGTACTCGCGCGGACACGC 1713
Db 30 TAAGTACTCGCGCGGACACGC 7

RESULT 47
LOCUS CQ403310/c 312 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 10381 from Patent WO0170979.
ACCESSION CQ403310
VERSION CQ403310.1 GI:41311091
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 10381 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
1. .312
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 24; DB 6; Length 312;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1690 TAAGTACTCGCGCGGACACGC 1713
Db 30 TAAGTACTCGCGCGGACACGC 7

RESULT 48
LOCUS CQ395905/c 319 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 2976 from Patent WO0170979.
ACCESSION CQ395905
VERSION CQ395905.1 GI:41303686
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 2976 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
1. .319
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 24; DB 6; Length 319;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1690 TAAGTACTCGCGCGGACCGC 1713
LOCUS
Db 30 TAAGTACTCGCGCGGACCGC 7

RESULT 49
CQ402234/c
LOCUS
DEFINITION Sequence 9305 from Patent WO0170979.
ACCESSION CQ402234
VERSION CQ402234.1 GI:41310015
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
1
Lee, J. and Lillie, J.
Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 9305 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1..319
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCGCGCGGACCGC 1713
LOCUS
Db 30 TAAGTACTCGCGCGGACCGC 7

RESULT 50
CQ410876/c
LOCUS
DEFINITION Sequence 17947 from Patent WO0170979.
ACCESSION CQ410876
VERSION CQ410876.1 GI:41318657
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
1
Lee, J. and Lillie, J.
Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 17947 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1..326
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 326;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCGCGCGGACCGC 1713
LOCUS
Db 113 TAAGTACTCGCGCGGACCGC 90

RESULT 51
AX185234/c
LOCUS
DEFINITION Sequence 929 from Patent WO0142467.
ACCESSION AX185234
VERSION AX185234.1 GI:15136619
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
1
Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
Patent: WO 0142467-A 929 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source Location/Qualifiers
1..331
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCGCGCGGACCGC 1713
LOCUS
Db 30 TAAGTACTCGCGCGGACCGC 7

RESULT 52
CQ420511/c
LOCUS
DEFINITION Sequence 5545 from Patent WO0151628.
ACCESSION CQ420511
VERSION CQ420511.1 GI:41372740
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
1
Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of breast cancer
Patent: WO 0151628-A 5545 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1..337
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCGCGCGGACCGC 1713
LOCUS
Db 30 TAAGTACTCGCGCGGACCGC 7

RESULT 53
AX185287/c
LOCUS
DEFINITION Sequence 982 from Patent WO0142467.
ACCESSION AX185287

VERSION AX185287.1 GI:15136675
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
TITLE Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 982 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES source
Location/Qualifiers
1..338
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 338;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGACACGCG 1713
Db 30 TAAGTACTCGCGCGACACGCG 7
RESULT 54
LOCUS CQ476128 346 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 7995 from Patent WO0160860.
ACCESSION CQ476128
VERSION CQ476128.1 GI:41441747
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 7995 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES source
Location/Qualifiers
1..346
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 346;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGACACGCG 1713
Db 30 TAAGTACTCGCGCGACACGCG 7
RESULT 55
LOCUS CQ397640 368 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 4711 from Patent WO0170979.
ACCESSION CQ397640
VERSION CQ397640.1 GI:41305421
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 4711 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES source
Location/Qualifiers
1..368
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/db_xref="taxon:9606"
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Query Match 1.4%; Score 24; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGACACGCG 1713
Db 30 TAAGTACTCGCGCGACACGCG 7
RESULT 56
LOCUS CQ403939 368 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 11010 from Patent WO0170979.
ACCESSION CQ403939
VERSION CQ403939.1 GI:41311720
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 11010 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES source
Location/Qualifiers
1..368
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGACACGCG 1713
Db 30 TAAGTACTCGCGCGACACGCG 7
RESULT 57
LOCUS CQ398887 370 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 5958 from Patent WO0170979.
ACCESSION CQ398887
VERSION CQ398887.1 GI:41306668
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,

JOURNAL assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 5958 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source
1..370
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 1.4%; Score 24; DB 6; Length 370;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCTCGCGCGACCGC 1713
|||||
Db 30 TAAGTACTCTCGCGCGACCGC 7

RESULT 58
CQ405167/c
LOCUS 370 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 12238 from Patent WO0170979.
ACCESSION CQ405167
VERSION CQ405167.1 GI:41312948
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 12238 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source
1..370
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 370;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCTCGCGCGACCGC 1713
|||||
Db 30 TAAGTACTCTCGCGCGACCGC 7

RESULT 59
CQ474199/c
LOCUS 376 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 6066 from Patent WO0160860.
ACCESSION CQ474199
VERSION CQ474199.1 GI:41439818
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 2902 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source
1..376
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 376;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 376;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCTCGCGCGACCGC 1713
|||||
Db 30 TAAGTACTCTCGCGCGACCGC 7

RESULT 60
CQ409694/c
LOCUS 382 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 16765 from Patent WO0170979.
ACCESSION CQ409694
VERSION CQ409694.1 GI:41317475
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 16765 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCTCGCGCGACCGC 1713
|||||
Db 101 TAAGTACTCTCGCGCGACCGC 78

RESULT 61
CQ395831/c
LOCUS 391 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 2902 from Patent WO0170979.
ACCESSION CQ395831
VERSION CQ395831.1 GI:41303612
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 2902 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source
1..391
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 1.4%; Score 24; DB 6; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCGCGCGACACGC 1713
Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 62
LOCUS CQ402160 391 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 9231 from Patent WO0170979.
ACCESSION CQ402160
VERSION CQ402160.1 GI:41309941
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 9231 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..391
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 1.4%; Score 24; DB 6; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCGCGCGACACGC 1713
Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 63
LOCUS CQ409304 391 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 16375 from Patent WO0170979.
ACCESSION CQ409304
VERSION CQ409304.1 GI:41317085
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 16375 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..391
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 1.4%; Score 24; DB 6; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCGCGCGACACGC 1713

Db 110 TAAGTACTCGCGCGACACGC 87

RESULT 64
LOCUS CQ396196 392 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 3267 from Patent WO0170979.
ACCESSION CQ396196
VERSION CQ396196.1 GI:41303977
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 3267 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..392
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 1.4%; Score 24; DB 6; Length 392;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCGCGCGACACGC 1713
Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 65
LOCUS CQ402521 392 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 9592 from Patent WO0170979.
ACCESSION CQ402521
VERSION CQ402521.1 GI:41310302
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 9592 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"

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Query Match 1.4%; Score 24; DB 6; Length 392;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCGCGCGACACGC 1713
Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 66

CQ476176/c
LOCUS CQ476176 404 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 8043 from Patent WO0160860.
ACCESSION CQ476176
VERSION CQ476176.1 GI:41441795
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS 1
TITLE Schlegel, R., Endege, W.O. and Monahan, J.E.
JOURNAL Genes differentially expressed in human prostate cancer and their
FEATURES use
source Patent: WO 0160860-A 8043 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTCGCGCGACACGC 1713
Db 30 TAAGTACTCTCGCGCGACACGC 7
RESULT 67
CQ408978/c
LOCUS CQ408978 409 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 16049 from Patent WO0170979.
ACCESSION CQ408978
VERSION CQ408978.1 GI:41316759
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS 1
TITLE Lee, J. and Lillie, J.
JOURNAL Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 16049 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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/db_xref="taxon:9606"
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 111 TAAGTACTCTCGCGCGACACGC 88
RESULT 68
CQ410088/c
LOCUS CQ410088 415 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 17159 from Patent WO0170979.
ACCESSION CQ410088
VERSION CQ410088.1 GI:41317869

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS 1
TITLE Lee, J. and Lillie, J.
JOURNAL Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 17159 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..415
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTCGCGCGACACGC 1713
Db 111 TAAGTACTCTCGCGCGACACGC 88
RESULT 69
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LOCUS CQ398150 416 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 5221 from Patent WO0170979.
ACCESSION CQ398150
VERSION CQ398150.1 GI:41305931
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS 1
TITLE Lee, J. and Lillie, J.
JOURNAL Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 5221 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..416
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTCGCGCGACACGC 1713
Db 30 TAAGTACTCTCGCGCGACACGC 7
RESULT 70
CQ404437/c
LOCUS CQ404437 416 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 11508 from Patent WO0170979.
ACCESSION CQ404437
VERSION CQ404437.1 GI:41312218
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 11508 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 30 TAAGTACTCGCGCGGACCAACGC 7
RESULT 71
LOCUS CQ405708 420 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 12779 from Patent WO0170979.
ACCESSION CQ405708
VERSION CQ405708.1 GI:41313489
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 12779 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 391 TAAGTACTCGCGCGGACCAACGC 414
RESULT 72
LOCUS CQ408618 420 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 15689 from Patent WO0170979.
ACCESSION CQ408618
VERSION CQ408618.1 GI:41316399
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer

JOURNAL Patent: WO 0170979-A 15689 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGGACCAACGC 1713
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RESULT 73
LOCUS CQ398742 421 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 5813 from Patent WO0170979.
ACCESSION CQ398742
VERSION CQ398742.1 GI:41306523
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 5813 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
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Qy 1690 TAAGTACTCGCGCGGACCAACGC 1713
Db 391 TAAGTACTCGCGCGGACCAACGC 414
RESULT 74
LOCUS CQ507382 424 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 39249 from Patent WO0160860.
ACCESSION CQ507382
VERSION CQ507382.1 GI:41473592
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their use
JOURNAL Patent: WO 0160860-A 39249 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACCGC 1713
Db 85 TAAGTACTCGCGCGGACCGC 62

RESULT 75
CO411425/c
LOCUS CO411425 426 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 18496 from Patent WO0170979.
ACCESSION CO411425
VERSION CO411425.1 GI:41319206
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 18496 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 111 TAAGTACTCGCGCGGACCGC 88

RESULT 76
CO474699/c
LOCUS CO474699 426 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 6566 from Patent WO0160860.
ACCESSION CO474699
VERSION CO474699.1 GI:41440318
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 6566 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 111 TAAGTACTCGCGCGGACCGC 88

RESULT 76
CO474699/c
LOCUS CO474699 426 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 6566 from Patent WO0160860.
ACCESSION CO474699
VERSION CO474699.1 GI:41440318
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 6566 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
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RESULT 76
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LOCUS CO474699 426 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 6566 from Patent WO0160860.
ACCESSION CO474699
VERSION CO474699.1 GI:41440318
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
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AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 6566 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
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Qy 1690 TAAGTACTCGCGCGGACCGC 1713
Db 95 TAAGTACTCGCGCGGACCGC 72

RESULT 77
CO411551/c
LOCUS CO411551 432 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 18622 from Patent WO0170979.
ACCESSION CO411551
VERSION CO411551.1 GI:41319332
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 18622 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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Db 95 TAAGTACTCGCGCGGACCGC 72

RESULT 78
CO506077/c
LOCUS CO506077 432 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 37944 from Patent WO0160860.
ACCESSION CO506077
VERSION CO506077.1 GI:41472201
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 37944 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
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ORIGIN
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DEFINITION  Sequence 3100 from Patent WO0170979.
ACCESSION   CQ396029
VERSION     CQ396029.1 GI:41303810
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1
AUTHORS    Lee, J. and Lillie, J.
TITLE      Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL    Patent: WO 0170979-A 3100 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 80
LOCUS       CQ402355/c
DEFINITION  Sequence 9426 from Patent WO0170979.
ACCESSION   CQ402355
VERSION     CQ402355.1 GI:41310136
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1
AUTHORS    Lee, J. and Lillie, J.
TITLE      Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL    Patent: WO 0170979-A 9426 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 79
LOCUS       CQ396029/c
DEFINITION  Sequence 3100 from Patent WO0170979.
ACCESSION   CQ396029
VERSION     CQ396029.1 GI:41318726
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1
AUTHORS    Lee, J. and Lillie, J.
TITLE      Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL    Patent: WO 0170979-A 18016 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
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RESULT 82
LOCUS       CQ408774/c
DEFINITION  Sequence 15845 from Patent WO0170979.
ACCESSION   CQ408774
VERSION     CQ408774.1 GI:41316555
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1
AUTHORS    Lee, J. and Lillie, J.
TITLE      Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL    Patent: WO 0170979-A 15845 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 83
LOCUS       CQ397235/c
DEFINITION  Sequence 4306 from Patent WO0170979.
ACCESSION   CQ397235
VERSION     CQ397235.1 GI:41305016
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 4306 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7
RESULT 84
CO403539/c
LOCUS CQ403539 446 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 10610 from Patent WO0170979.
ACCESSION CQ403539
VERSION CQ403539.1 GI:41311320
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 10610 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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Db 30 TAAGTACCTCGCGCGGACACGC 7
RESULT 85
CO504192/c
LOCUS CQ504192 446 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 36059 from Patent WO0160860.
ACCESSION CQ504192
VERSION CQ504192.1 GI:41470221
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 36059 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
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Db 101 TAAGTACCTCGCGCGGACACGC 78
RESULT 86
CO506124/c
LOCUS CQ506124 446 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 37991 from Patent WO0160860.
ACCESSION CQ506124
VERSION CQ506124.1 GI:41472250
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 37991 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES Location/Qualifiers
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Db 71 TAAGTACCTCGCGCGGACACGC 48
RESULT 87
CO513253/c
LOCUS CQ513253 446 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 45120 from Patent WO0160860.
ACCESSION CQ513253
VERSION CQ513253.1 GI:41479517
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 45120 23-AUG-2001;

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Db 101 TAAGTACCTCGCGCGGACACGCG 78

RESULT 88
LOCUS      KPN293850/c 450 bp DNA linear BCT 24-NOV-2000
DEFINITION Klebsiella pneumoniae partial EVGA gene for putative positive
transcription regulator EVGA, contig region pSL042.
ACCESSION AJ293850
VERSION AJ293850.1 GI:9909726
KEYWORDS EVGA gene; positive transcription regulator EVGA.
SOURCE Klebsiella pneumoniae
ORGANISM Klebsiella pneumoniae
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
REFERENCE 1
AUTHORS Lai, Y.C., Yang, S.L., Peng, H.L. and Chang, H.Y.
TITLE Identification of genes present specifically in a virulent strain
of Klebsiella pneumoniae
JOURNAL Infect. Immun. 68 (12), 7149-7151 (2000)
PUBMED 11083844
REFERENCE 2 (bases 1 to 450)
AUTHORS Yang, S.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Yang S., Life Science, National Tsing Hua
University, 101, Section 2 Kuang Fu Road, Hsinchu, 300, TAIWAN

FEATURES
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    /country="Taiwan"
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Qy 1690 TAAGTACCTCGCGCGGACACGCG 1713
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Db 108 TAAGTACCTCGCGCGGACACGCG 85

RESULT 91
LOCUS      CQ396273/c 464 bp DNA linear PAT 23-JAN-2004
DEFINITION Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
TITLE Compositions and methods relating to lung specific genes and
proteins
JOURNAL Patent: WO 02064788-A 66 22-AUG-2002;
Diadexus, Inc. (US)
FEATURES
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Db 24 TAAGTACCTCGCGCGGACACGCG 1

RESULT 90
LOCUS      CQ411634/c 460 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 18705 from Patent WO0170979.
ACCESSION CQ411634
VERSION CQ411634.1 GI:41319415
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 18705 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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Qy 1690 TAAGTACCTCGCGCGGACACGCG 1713
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Db 108 TAAGTACCTCGCGCGGACACGCG 85

RESULT 91
LOCUS      CQ396273/c 464 bp DNA linear PAT 23-JAN-2004
DEFINITION Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
TITLE Compositions and methods relating to lung specific genes and
proteins
JOURNAL Patent: WO 02064788-A 66 22-AUG-2002;
Diadexus, Inc. (US)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 3344 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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/db_xref="taxon:9606"
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Db 30 TAAGTACTCGCGCGGACCAACGC 7
RESULT 92
CQ402594/c
LOCUS CQ402594 464 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 9665 from Patent WO0170979.
ACCESSION CQ402594
VERSION CQ402594.1 GI:41310375
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 9665 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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Db 30 TAAGTACTCGCGCGGACCAACGC 7
RESULT 93
CQ408780/c
LOCUS CQ408780 471 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 15851 from Patent WO0170979.
ACCESSION CQ408780
VERSION CQ408780.1 GI:41316561
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 472 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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Db 30 TAAGTACTCGCGCGGACCAACGC 7
RESULT 94
CQ397401/c
LOCUS CQ397401 486 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 4472 from Patent WO0170979.
ACCESSION CQ397401
VERSION CQ397401.1 GI:41305182
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 4472 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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DEFINITION Sequence 10775 from Patent WO0170979.
ACCESSION CQ403704
VERSION CQ403704.1 GI:41311485
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
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TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 10775 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)

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RESULT 96

AX185141/c
LOCUS AX185141 500 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 836 from Patent WO0142467.
ACCESSION AX185141
VERSION AX185141.1 GI:15136522

KEYWORDS

source Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 Schlegel R., Deeds J., Berger A. and Zhao X.
Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer
Patent: WO 0142467-A 836 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)

FEATURES

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Db 30 TAAGTACTCGCGCGGACCAACGC 7

RESULT 97

CQ409296/c
LOCUS CQ409296 503 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 16367 from Patent WO0170979.
ACCESSION CQ409296
VERSION CQ409296.1 GI:41317077

KEYWORDS

source Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 Lee, J. and Lillie, J.
Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 16367 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)

FEATURES

Location/Qualifiers

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CQ408905/c
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DEFINITION Sequence 15976 from Patent WO0170979.
ACCESSION CQ408905
VERSION CQ408905.1 GI:41316686

KEYWORDS

source Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 Lee, J. and Lillie, J.
Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 15976 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)

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CQ397922/c
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DEFINITION Sequence 4993 from Patent WO0170979.
ACCESSION CQ397922
VERSION CQ397922.1 GI:41305703

KEYWORDS

source Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 Lee, J. and Lillie, J.
Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 4993 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)

FEATURES

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 DB 30 TAAGTACCTCGCGCGGACCGC 7

RESULT 100
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 DEFINITION Sequence 11286 from Patent WO0170979.

ACCESSION CO404215
 VERSION CO404215.1 GI:41311996

KEYWORDS
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1
 AUTHORS Lee, J. and Lillie, J.
 TITLE Genes, compositions, kits, and method for identification,
 assessment, prevention, and therapy of ovarian cancer
 JOURNAL Patent: WO 0170979-A 11286 27-SEP-2001;
 Millennium Pharmaceuticals, Inc. (US)

FEATURES
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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SUMMARIES

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5	983	57.4	1977	6	ABX92014
6	683	39.9	791	14	AEA19545
7	385	22.5	385	6	ABX92013
8	378	22.1	386	6	ABT07644
9	378	22.1	386	8	ABT13389
10	334	19.5	393	5	AAF64421
11	321	18.7	427	5	AAF66376
12	300	17.5	300	2	AZ13392
13	249	14.5	300	2	AAx98308
14	222	13.0	654	6	ABX92074
15	120	7.0	120	6	ABX92074
16	38	2.2	728	2	Az117414
17	28	1.6	323	4	AAH69926
18	28	1.6	329	4	AAH69438
19	26	1.5	91	5	AAF98612

Aah70084	Human cer	203	4	AAH70084
Aah70907	Human cer	412	4	AAH70907
Aal17411	Human bre	576	4	AAL17411
Abz08482	Human leu	224	6	ABZ08482
Abv37465	Human pro	255	5	ABV37465
Adi43520	Human ova	275	5	ADL43520
Abv07533	Human pro	304	5	ABV07533
Adi37497	Human ova	310	5	ADL37497
Adi72353	Human ova	310	5	ADL72353
Aal14408	Human bre	358	4	AAL14408
Aah69711	Human cer	359	4	AAH69711
Abv98985	Human pan	453	6	ABV98985
Adi43881	Human ova	463	5	ADL43881
Abz67274	Breast sp	810	6	ABS67274
Acn84455	Breast ca	1252	11	ACN84455
Ady99697	T reesei	150	14	ADY99697
Abt23431	Immune-re	232	8	ABT23431
Adi43332	Human ova	253	5	ADL43332
Adi37742	Human ova	274	5	ADL37742
Adi72603	Human ova	274	5	ADL72603
Adi42505	Human ova	283	5	ADL42505
Adi70936	Human ova	310	5	ADL70936
Adi77249	Human ova	310	5	ADL77249
Adi36491	Human ova	312	5	ADL36491
Adi71332	Human ova	312	5	ADL71332
Adi70234	Human ova	319	5	ADL70234
Adi76563	Human ova	319	5	ADL76563
Abq58175	Human col	320	6	ABQ58175
Adl44057	Human ova	326	5	ADL44057
Aah69655	Human cer	331	4	AAH69655
Aal13080	Human bre	337	4	AAL13080
Aah69708	Human cer	338	4	AAH69708
Abv08004	Human pro	346	5	ABV08004
Adi37120	Human ova	368	5	ADL37120
Adi71969	Human ova	368	5	ADL71969
Adi73216	Human ova	370	5	ADL73216
Adi38348	Human ova	370	5	ADL38348
Abv06075	Human pro	376	5	ABV06075
Adl42875	Human ova	382	5	ADL42875
Adi76489	Human ova	391	5	ADL76489
Adi70160	Human ova	391	5	ADL70160
Adi42485	Human ova	391	5	ADL42485
Adi76850	Human ova	392	5	ADL76850
Adi70525	Human ova	392	5	ADL70525
Abv08052	Human pro	404	5	ABV08052
Adl42159	Human ova	409	5	ADL42159
Adi43269	Human ova	415	5	ADL43269
Adi37618	Human ova	416	5	ADL37618
Adi72479	Human ova	416	5	ADL72479
Adi38889	Human ova	420	5	ADL38889
Adl41799	Human ova	420	5	ADL41799
Adi73071	Human ova	421	5	ADL73071
Abv39230	Human pro	424	5	ABV39230
Acn86430	Breast ca	425	11	ACN86430
Abv06575	Human pro	426	5	ABV06575
Adl44606	Human ova	426	5	ADL44606
Abv37925	Human pro	432	5	ABV37925
Adl44732	Human ova	432	5	ADL44732
Adi70358	Human ova	437	5	ADL70358
Adi76684	Human ova	437	5	ADL76684
Adl44126	Human ova	444	5	ADL44126
Adl41955	Human ova	444	5	ADL41955
Abv36041	Human pro	446	5	ABV36041
Abv37972	Human pro	446	5	ABV37972
Abv45101	Human pro	446	5	ABV45101
Adi36720	Human ova	446	5	ADL36720
Adi71564	Human ova	446	5	ADL71564
Abai1128	Human ner	449	5	ABAI1128
Abq75327	Human lun	457	6	ABQ75327
Adl44815	Human ova	460	5	ADL44815
Acn84351	Breast ca	463	11	ACN84351
Adi70602	Human ova	464	5	ADL70602
Adi76923	Human ova	464	5	ADL76923

C 93	24	1.4	471	5	ADL41961	Human ova	Adl41961	Human ova	C 166	23	1.3	142	5	ABV37788	Human pro	Abv37788	Human pro
C 94	24	1.4	486	5	ADL36885	Human ova	Adl36885	Human ova	C 167	23	1.3	142	5	ADI71927	Human ova	Adi71927	Human ova
C 95	24	1.4	486	5	ADI71730	Human ova	Adi71730	Human ova	C 168	23	1.3	142	5	ADL37078	Human ova	Adl37078	Human ova
C 96	24	1.4	500	4	AAH69562	Human cer	Aah69562	Human cer	C 169	23	1.3	143	5	ADL44859	Human ova	Adl44859	Human ova
C 97	24	1.4	503	5	ADL42477	Human ova	Adl42477	Human ova	C 170	23	1.3	143	5	ADL37494	Human ova	Adl37494	Human ova
C 98	24	1.4	517	5	ADL42086	Human ova	Adl42086	Human ova	C 171	23	1.3	147	5	ADI72350	Human ova	Adi72350	Human ova
C 99	24	1.4	521	5	ADI72251	Human ova	Adi72251	Human ova	C 172	23	1.3	147	14	ADY99160	T reesei	Ady99160	T reesei
C 100	24	1.4	521	5	ADL41725	Human ova	Adl41725	Human ova	C 173	23	1.3	149	5	ABV07432	Human pro	Abv07432	Human pro
C 101	24	1.4	521	5	ADL37396	Human ova	Adl37396	Human ova	C 174	23	1.3	149	5	ADL37926	Human ova	Adl37926	Human ova
C 102	24	1.4	524	4	AAH69765	Human cer	Aah69765	Human cer	C 175	23	1.3	149	5	ADI72787	Human ova	Adi72787	Human ova
C 103	24	1.4	524	5	ADL44002	Human ova	Adl44002	Human ova	C 176	23	1.3	150	5	ABV37344	Human pro	Abv37344	Human pro
C 104	24	1.4	529	4	AAH14398	Human bre	Aah14398	Human bre	C 177	23	1.3	150	5	ADL43256	Human ova	Adl43256	Human ova
C 105	24	1.4	534	5	ADL38215	Human ova	Adl38215	Human ova	C 178	23	1.3	151	5	ADL38426	Human ova	Adl38426	Human ova
C 106	24	1.4	534	5	ADI73081	Human ova	Adi73081	Human ova	C 179	23	1.3	151	5	ADI73295	Human ova	Adi73295	Human ova
C 107	24	1.4	546	5	ADL43504	Human ova	Adl43504	Human ova	C 180	23	1.3	153	4	RAA07787	Cervical	Aas07787	Cervical
C 108	24	1.4	548	5	ADI73300	Human ova	Adi73300	Human ova	C 181	23	1.3	156	5	ADI72273	Human ova	Adi72273	Human ova
C 109	24	1.4	548	5	ADL38431	Human ova	Adl38431	Human ova	C 182	23	1.3	156	5	ADL37417	Human ova	Adl37417	Human ova
C 110	24	1.4	569	5	ABV39377	Human pro	Abv39377	Human pro	C 183	23	1.3	157	4	RAA15947	Human bre	Aal15947	Human bre
C 111	24	1.4	569	5	ABV43977	Human pro	Abv43977	Human pro	C 184	23	1.3	157	14	ADY99268	T reesei	Ady99268	T reesei
C 112	24	1.4	601	5	ADL44599	Human ova	Adl44599	Human ova	C 185	23	1.3	160	4	AA07814	Cervical	Aas07814	Cervical
C 113	24	1.4	610	5	ABV45091	Human pro	Abv45091	Human pro	C 186	23	1.3	162	4	RAA16016	Human bre	Aal16016	Human bre
C 114	24	1.4	610	5	ABV36031	Human pro	Abv36031	Human pro	C 187	23	1.3	162	4	AAH69981	Human cer	Aah69981	Human cer
C 115	24	1.4	610	14	ADY98758	T reesei	Ady98758	T reesei	C 188	23	1.3	167	5	ABV37696	Human pro	Abv37696	Human pro
C 116	24	1.4	619	5	ADL43780	Human ova	Adl43780	Human ova	C 189	23	1.3	167	5	AAH69074	Human pro	Aah69074	Human pro
C 117	24	1.4	628	5	ADL43760	Human ova	Adl43760	Human ova	C 190	23	1.3	168	4	AAH69848	Human cer	Aah69848	Human cer
C 118	24	1.4	629	5	ADL43104	Human ova	Adl43104	Human ova	C 191	23	1.3	168	5	ADI71514	Human ova	Adi71514	Human ova
C 119	24	1.4	638	5	ADL45048	Human ova	Adl45048	Human ova	C 192	23	1.3	168	5	ADL36670	Human ova	Adl36670	Human ova
C 120	24	1.4	646	5	ADI72596	Human ova	Adi72596	Human ova	C 193	23	1.3	169	5	ABV37535	Human pro	Abv37535	Human pro
C 121	24	1.4	646	5	ADL37735	Human ova	Adl37735	Human ova	C 194	23	1.3	170	4	RAA13007	Human bre	Aal13007	Human bre
C 122	24	1.4	658	11	ACN88035	Breast ca	Acn88035	Breast ca	C 195	23	1.3	170	4	AAH70047	Human cer	Aah70047	Human cer
C 123	24	1.4	687	5	ADL44374	Human ova	Adl44374	Human ova	C 196	23	1.3	170	5	ABV07357	Human pro	Abv07357	Human pro
C 124	24	1.4	739	5	ADL36121	Human ova	Adl36121	Human ova	C 197	23	1.3	170	6	ABZ08159	Human leu	Abz08159	Human leu
C 125	24	1.4	739	5	ADI70957	Human ova	Adi70957	Human ova	C 198	23	1.3	170	14	ADY99153	T reesei	Ady99153	T reesei
C 126	24	1.4	757	5	ABV09078	Human pro	Abv09078	Human pro	C 199	23	1.3	172	5	ABV37319	Human ova	Abv37319	Human ova
C 127	24	1.4	818	6	ABQ66927	Human exp	Abq66927	Human exp	C 200	23	1.3	172	5	ADL38611	Human ova	Adl38611	Human ova
C 128	24	1.4	872	11	ACN83198	Breast ca	Acn83198	Breast ca	C 201	23	1.3	172	5	ADI73481	Human ova	Adi73481	Human ova
C 129	24	1.4	894	11	ACN84445	Breast ca	Acn84445	Breast ca	C 202	23	1.3	174	5	ABV37373	Human pro	Abv37373	Human pro
C 130	23	1.3	42	10	ABT23040	Breast ca	Abt23040	Breast ca	C 203	23	1.3	174	5	ABV07688	Human pro	Abv07688	Human pro
C 131	23	1.3	43	4	AA077704	Cervical	Aas077704	Cervical	C 204	23	1.3	174	10	ABT22983	Breast ca	Abt22983	Breast ca
C 132	23	1.3	45	10	ABT22680	Breast ca	Abt22680	Breast ca	C 205	23	1.3	176	5	ABV07603	Human pro	Abv07603	Human pro
C 133	23	1.3	45	4	AA077717	Cervical	Aas077717	Cervical	C 206	23	1.3	176	5	ADL44941	Human ova	Adl44941	Human ova
C 134	23	1.3	46	10	ABT23042	Breast ca	Abt23042	Breast ca	C 207	23	1.3	177	4	AAH70129	Human cer	Aah70129	Human cer
C 135	23	1.3	54	4	AA077761	Cervical	Aas077761	Cervical	C 208	23	1.3	177	5	ABV35931	Human ova	Abv35931	Human ova
C 136	23	1.3	60	4	AA077762	Cervical	Aas077762	Cervical	C 209	23	1.3	177	5	ADL36883	Human ova	Adl36883	Human ova
C 137	23	1.3	79	4	AA077781	Cervical	Aas077781	Cervical	C 210	23	1.3	177	5	ADI71728	Human ova	Adi71728	Human ova
C 138	23	1.3	82	5	AAAF98632	Human ova	Aaf98632	Human ova	C 211	23	1.3	177	5	ADL44790	Human ova	Adl44790	Human ova
C 139	23	1.3	83	5	AAAF98670	Human ova	Aaf98670	Human ova	C 212	23	1.3	177	5	ADI71828	Human ova	Adi71828	Human ova
C 140	23	1.3	85	4	AA07817	Cervical	Aas07817	Cervical	C 213	23	1.3	177	5	ADL36981	T reesei	Adl36981	T reesei
C 141	23	1.3	88	5	ADL45036	Human ova	Adl45036	Human ova	C 214	23	1.3	177	14	ADY99639	T reesei	Ady99639	T reesei
C 142	23	1.3	92	4	AA07811	Cervical	Aas07811	Cervical	C 215	23	1.3	178	5	ABV08201	Human pro	Abv08201	Human pro
C 143	23	1.3	92	5	ADL44388	Human ova	Adl44388	Human ova	C 216	23	1.3	178	5	ADL38728	Human ova	Adl38728	Human ova
C 144	23	1.3	94	14	ADY99584	T reesei	Ady99584	T reesei	C 217	23	1.3	178	5	ADI73598	Human ova	Adi73598	Human ova
C 145	23	1.3	96	5	ADL44706	Human ova	Adl44706	Human ova	C 218	23	1.3	179	4	AAH70006	Human cer	Aah70006	Human cer
C 146	23	1.3	103	5	ABV07864	Human pro	Abv07864	Human pro	C 219	23	1.3	179	5	ADI72023	Human ova	Adi72023	Human ova
C 147	23	1.3	104	10	ABT23029	Breast ca	Abt23029	Breast ca	C 220	23	1.3	179	5	ADL37172	Human ova	Adl37172	Human ova
C 148	23	1.3	111	4	AA077743	Cervical	Aas077743	Cervical	C 221	23	1.3	179	14	ADY99505	T reesei	Ady99505	T reesei
C 149	23	1.3	114	5	ABV37291	Human pro	Abv37291	Human pro	C 222	23	1.3	180	5	ABV07358	Human pro	Abv07358	Human pro
C 150	23	1.3	115	5	ABAl1124	Human ner	Abal1124	Human ner	C 223	23	1.3	181	5	ABV38094	Human pro	Abv38094	Human pro
C 151	23	1.3	116	5	AAAF98624	Human ova	Aaf98624	Human ova	C 224	23	1.3	181	5	ADL44184	Human ova	Adl44184	Human ova
C 152	23	1.3	117	14	ADY99491	T reesei	Ady99491	T reesei	C 225	23	1.3	183	5	ADI71856	Human ova	Adi71856	Human ova
C 153	23	1.3	119	4	AA077746	Cervical	Aas077746	Cervical	C 226	23	1.3	183	5	ADL37007	Human ova	Adl37007	Human ova
C 154	23	1.3	120	4	AAH70046	Human cer	Aah70046	Human cer	C 227	23	1.3	184	5	ABV37315	Human pro	Abv37315	Human pro
C 155	23	1.3	120	5	AAAF98629	Human ova	Aaf98629	Human ova	C 228	23	1.3	186	5	ABV38136	Human pro	Abv38136	Human pro
C 156	23	1.3	122	10	ABT22949	Breast ca	Abt22949	Breast ca	C 229	23	1.3	187	5	ABV07994	Human pro	Abv07994	Human pro
C 157	23	1.3	127	5	ADL38453	Human ova	Adl38453	Human ova	C 230	23	1.3	187	5	ABV37710	Human pro	Abv37710	Human pro
C 158	23	1.3	127	5	ADI73322	Human ova	Adi73322	Human ova	C 231	23	1.3	188	4	AAH69871	Human cer	Aah69871	Human cer
C 159	23	1.3	128	4	AAH16208	Human bre	Aah16208	Human bre	C 232	23	1.3	188	5	ABV07594	Human pro	Abv07594	Human pro
C 160	23	1.3	128	5	ADI72310	Human ova	Adi72310	Human ova	C 233	23	1.3	188	5	ADL38023	Human ova	Adl38023	Human ova
C 161	23	1.3	128	5	ADL37454	Human ova	Adl37454	Human ova	C 234	23	1.3	188	5	ADI72884	Human ova	Adi72884	Human ova
C 162	23	1.3	133	5	ADI72651	Human ova	Adi72651	Human ova	C 235	23	1.3	189	4	RAA15994	Human bre	Aal15994	Human bre
C 163	23	1.3	133	5	ADL37790	Human ova	Adl37790	Human ova	C 236	23	1.3	189	5	ADL42273	Human ova	Adl42273	Human ova
C 164	23	1.3	136	5	ABV07461	Human pro	Abv07461	Human pro	C 237	23	1.3	190	5	ABV37682	Human pro	Abv37682	Human pro
C 165	23	1.3	140	5	ADL43524	Human ova	Adl43524	Human ova	C 238	23	1.3	190	5	ADI77194	Human ova	Adi77194	Human ova

C 239	1.3	190	5	ADI70880	Adi70880 Human ova	C 312	23	1.3	245	11	ADT94522	Adt94522 Colon can
C 240	1.3	191	5	ABV07340	Abv07340 Human pro	C 313	23	1.3	245	11	ADX41004	Adx41004 Human CDN
C 241	1.3	191	5	ADL44602	Adl44602 Human ova	C 314	23	1.3	246	4	AAH69927	Aah69927 Human cer
C 242	1.3	193	5	ABV37615	Abv37615 Human pro	C 315	23	1.3	246	5	ADL72681	Adl72681 Human ova
C 243	1.3	194	4	AAH70137	Aah70137 Human cer	C 316	23	1.3	246	5	ADL37820	Adl37820 Human ova
C 244	1.3	195	5	ABV37466	Abv37466 Human pro	C 317	23	1.3	247	5	ADL44864	Adl44864 Human ova
C 245	1.3	195	5	ADI73063	Adi73063 Human ova	C 318	23	1.3	247	14	ADY99362	Ady99362 T_reesei
C 246	1.3	195	5	ADI38198	Adi38198 Human ova	C 319	23	1.3	248	5	ADI72316	Adi72316 Human ova
C 247	1.3	195	5	ADI44837	Adi44837 Human ova	C 320	23	1.3	248	5	ADL44051	Adl44051 Human ova
C 248	1.3	196	5	ABV36903	Abv36903 Human pro	C 321	23	1.3	248	5	ADL37460	Adl37460 Human ova
C 249	1.3	196	5	ABV38080	Abv38080 Human pro	C 322	23	1.3	249	5	ADI73073	Adi73073 Human ova
C 250	1.3	198	4	AA507727	Aas07727 Cervical	C 323	23	1.3	249	5	ADL38207	Adl38207 Human ova
C 251	1.3	198	5	ADI72060	Adi72060 Human ova	C 324	23	1.3	250	5	ADI76910	Adi76910 Human ova
C 252	1.3	198	5	ADI37209	Adi37209 Human ova	C 325	23	1.3	250	5	ADI70589	Adi70589 Human ova
C 253	1.3	200	5	ABV08135	Abv08135 Human pro	C 326	23	1.3	250	14	ADY99318	Ady99318 T_reesei
C 254	1.3	200	5	ADI38653	Adi38653 Human ova	C 327	23	1.3	251	4	AAI13275	Aal13275 Human bre
C 255	1.3	200	5	ADI73523	Adi73523 Human ova	C 328	23	1.3	252	5	ABV38113	Abv38113 Human pro
C 256	1.3	203	5	ADI44849	Adi44849 Human ova	C 329	23	1.3	253	5	ABV08181	Abv08181 Human pro
C 257	1.3	203	5	ADI37929	Adi37929 Human ova	C 330	23	1.3	253	5	ADI72143	Adi72143 Human ova
C 258	1.3	203	5	ADI44881	Adi44881 Human ova	C 331	23	1.3	253	5	ADL37667	Adl37667 Human ova
C 259	1.3	203	5	ADI72790	Adi72790 Human ova	C 332	23	1.3	253	5	ADI72528	Adi72528 Human ova
C 260	1.3	205	5	ADI44359	Adi44359 Human ova	C 333	23	1.3	253	5	ADL37291	Adl37291 Human ova
C 261	1.3	206	4	ADL44537	Adl44537 Human ova	C 334	23	1.3	254	4	AAH70098	Aah70098 Human cer
C 262	1.3	207	4	AA507749	Aas07749 Cervical	C 335	23	1.3	254	4	AAH69930	Aah69930 Human cer
C 263	1.3	207	5	ABV07950	Abv07950 Human pro	C 336	23	1.3	254	5	ABV35993	Abv35993 Human pro
C 264	1.3	209	5	ABV07955	Abv07955 Human pro	C 337	23	1.3	255	5	AAH82158	Aah82158 Rat diffe
C 265	1.3	209	5	ADI38659	Adi38659 Human ova	C 338	23	1.3	255	5	AAH82061	Aah82061 Rat diffe
C 266	1.3	209	5	ADI73529	Adi73529 Human ova	C 339	23	1.3	255	5	ABV37771	Abv37771 Human pro
C 267	1.3	209	5	ADI77177	Adi77177 Human ova	C 340	23	1.3	257	4	AAH70066	Aah70066 Human cer
C 268	1.3	209	5	ADI70863	Adi70863 Human ova	C 341	23	1.3	257	4	AAH70073	Aah70073 Human cer
C 269	1.3	210	5	ADI44810	Adi44810 Human ova	C 342	23	1.3	257	5	ABV35942	Abv35942 Human pro
C 270	1.3	211	5	ABV37395	Abv37395 Human pro	C 343	23	1.3	257	5	ADL44735	Adl44735 Human ova
C 271	1.3	211	5	ABV08226	Abv08226 Human pro	C 344	23	1.3	257	12	ADP83360	Adp83360 Breast sp
C 272	1.3	212	4	AAH69501	Aah69501 Human cer	C 345	23	1.3	258	5	ABV37311	Abv37311 Human pro
C 273	1.3	212	10	ABT23044	Abt23044 Breast ca	C 346	23	1.3	258	5	ADI71975	Adi71975 Human ova
C 274	1.3	212	14	ADY99604	Ady99604 T_reesei	C 347	23	1.3	258	5	ADI72518	Adi72518 Human ova
C 275	1.3	212	5	ADI44591	Adi44591 Human ova	C 348	23	1.3	258	5	ADL37125	Adl37125 Human ova
C 276	1.3	214	5	ABV38022	Abv38022 Human pro	C 349	23	1.3	258	5	ADL37657	Adl37657 Human ova
C 277	1.3	217	5	ABV07377	Abv07377 Human pro	C 350	23	1.3	258	5	ABV37617	Abv37617 Human pro
C 278	1.3	219	4	AAH69486	Aah69486 Human cer	C 351	23	1.3	259	14	ADY99605	Ady99605 T_reesei
C 279	1.3	220	5	ABV07337	Abv07337 Human pro	C 352	23	1.3	260	4	AAI13303	Aal13303 Human bre
C 280	1.3	221	5	ADI44311	Adi44311 Human ova	C 353	23	1.3	260	5	ABV37366	Abv37366 Human pro
C 281	1.3	222	5	ADI43838	Adi43838 Human ova	C 354	23	1.3	260	5	ADL37961	Adl37961 Human ova
C 282	1.3	222	5	ADI44460	Adi44460 Human ova	C 355	23	1.3	260	5	ADI72822	Adi72822 Human ova
C 283	1.3	224	4	AAH69963	Aah69963 Human cer	C 356	23	1.3	260	12	ADL00209	Adl00209 Malignant
C 284	1.3	224	4	AAH69929	Aah69929 Human cer	C 357	23	1.3	261	5	ADI71099	Adi71099 Human ova
C 285	1.3	224	4	AAH69731	Aah69731 Human cer	C 358	23	1.3	261	5	ADL36260	Adl36260 Human ova
C 286	1.3	225	4	AAH70076	Aah70076 Human cer	C 359	23	1.3	263	5	ADI71894	Adi71894 Human ova
C 287	1.3	225	5	AAH69822	Aah69822 Human ova	C 360	23	1.3	263	5	ADL37045	Adl37045 Human ova
C 288	1.3	226	5	ADI72788	Adi72788 Human ova	C 361	23	1.3	264	4	AAI14372	Aal14372 Human bre
C 289	1.3	226	5	ADI73727	Adi73727 Human ova	C 362	23	1.3	264	5	ADL38218	Adl38218 Human ova
C 290	1.3	227	5	ABV07996	Abv07996 Human pro	C 363	23	1.3	264	5	ADI72366	Adi72366 Human ova
C 291	1.3	227	5	ADI73299	Adi73299 Human ova	C 364	23	1.3	264	5	ADI73084	Adi73084 Human ova
C 292	1.3	227	5	ADI38430	Adi38430 Human ova	C 365	23	1.3	264	5	ADL37510	Adl37510 Human ova
C 293	1.3	227	10	ABT22865	Abt22865 Breast ca	C 366	23	1.3	265	5	AAH69867	Aah69867 Human ova
C 294	1.3	231	5	ADI44202	Adi44202 Human ova	C 367	23	1.3	266	5	ABV36040	Abv36040 Human pro
C 295	1.3	232	5	ABV37391	Abv37391 Human pro	C 368	23	1.3	266	5	ABV45100	Abv45100 Human pro
C 296	1.3	234	5	ADI43326	Adi43326 Human ova	C 369	23	1.3	267	4	AAH69561	Aah69561 Human cer
C 297	1.3	235	4	AAI14545	Aal14545 Human bre	C 370	23	1.3	267	5	ABV37677	Abv37677 Human pro
C 298	1.3	235	5	AAH69890	Aah69890 Human cer	C 371	23	1.3	267	5	ABV37753	Abv37753 Human pro
C 299	1.3	235	5	ABV07568	Abv07568 Human pro	C 372	23	1.3	268	4	AAH70080	Aah70080 Human cer
C 300	1.3	235	5	ADI72022	Adi72022 Human ova	C 373	23	1.3	268	5	ABV69917	Abv69917 Human cer
C 301	1.3	235	5	ADI37171	Adi37171 Human ova	C 374	23	1.3	268	5	ABV38724	Abv38724 Human pro
C 302	1.3	235	5	ADI73143	Adi73143 Human ova	C 375	23	1.3	268	5	ADI73289	Adi73289 Human ova
C 303	1.3	235	5	ADI38276	Adi38276 Human ova	C 376	23	1.3	268	5	ADL38420	Adl38420 Human ova
C 304	1.3	236	10	ABT22889	Abt22889 Breast ca	C 377	23	1.3	269	4	AAI16395	Aal16395 Human bre
C 305	1.3	237	5	ABV07534	Abv07534 Human pro	C 378	23	1.3	269	4	AAH70096	Aah70096 Human cer
C 306	1.3	238	4	AA507775	Aas07775 Cervical	C 379	23	1.3	269	5	ABV08018	Abv08018 Human pro
C 307	1.3	238	4	AAH69502	Aah69502 Human cer	C 380	23	1.3	271	4	AAI16367	Aal16367 Human bre
C 308	1.3	241	5	ABV07986	Abv07986 Human pro	C 381	23	1.3	271	4	AAH70009	Aah70009 Human cer
C 309	1.3	241	5	ABV08250	Abv08250 Human pro	C 382	23	1.3	271	5	ADL43054	Adl43054 Human ova
C 310	1.3	241	14	ADY98867	Ady98867 T_reesei	C 383	23	1.3	271	5	ADL37357	Adl37357 Human ova
C 311	1.3	244	5	ABV07846	Abv07846 Human pro	C 384	23	1.3	271	5	ADL72212	Adl72212 Human ova

C 385	23	1.3	272	5	AD172411	Adi72411 Human ova
C 386	23	1.3	272	5	ADL37774	Adi37774 Human ova
C 387	23	1.3	272	5	ADL72635	Adi72635 Human ova
C 388	23	1.3	272	5	ADL37554	Adi37554 Human ova
C 389	23	1.3	273	5	ADL37629	Adi37629 Human ova
C 390	23	1.3	273	5	ADL72490	Adi72490 Human ova
C 391	23	1.3	273	6	ABV98946	Abv98946 Human pan
C 392	23	1.3	276	4	AA507741	Aas07741 Cervical
C 393	23	1.3	277	5	ABV37613	Abv37613 Human pro
C 394	23	1.3	277	5	ABV37936	Abv37936 Human pro
C 395	23	1.3	277	14	ADY98804	Ady98804 T_reesei
C 396	23	1.3	278	6	ABQ56327	Abq56327 Human col
C 397	23	1.3	279	5	ABV07457	Abv07457 Human pro
C 398	23	1.3	279	5	ADL38694	Adi38694 Human ova
C 399	23	1.3	279	5	ADL73564	Adi73564 Human ova
C 400	23	1.3	279	5	ADL43556	Adi43556 Human ova
C 401	23	1.3	281	5	ABV35976	Abv35976 Human pro
C 402	23	1.3	282	4	AA116353	Aal16353 Human bre
C 403	23	1.3	282	5	ABV08060	Abv08060 Human pro
C 404	23	1.3	282	5	ADL37122	Adi37122 Human ova
C 405	23	1.3	282	5	ADL38105	Adi38105 Human ova
C 406	23	1.3	282	5	ADI71972	Adi71972 Human ova
C 407	23	1.3	282	5	ADI72969	Adi72969 Human ova
C 408	23	1.3	283	5	ADI69337	Adi69337 Human ova
C 409	23	1.3	283	5	ADL44042	Adi44042 Human ova
C 410	23	1.3	283	5	ADI75681	Adi75681 Human ova
C 411	23	1.3	284	10	ABT22890	Abt22890 Breast ca
C 412	23	1.3	284	10	ABT22751	Abt22751 Breast ca
C 413	23	1.3	285	5	ABV37274	Abv37274 Human pro
C 414	23	1.3	285	12	ADQ18335	Adq18335 Human sof
C 415	23	1.3	285	14	ADY99470	Ady99470 T_reesei
C 416	23	1.3	287	5	ADL73568	Adi73568 Human ova
C 417	23	1.3	287	5	ADL38698	Adi38698 Human ova
C 418	23	1.3	287	5	ADI72856	Adi72856 Human ova
C 419	23	1.3	287	5	ADL37995	Adi37995 Human ova
C 420	23	1.3	287	14	ADY98677	Ady98677 T_reesei
C 421	23	1.3	288	4	AA507707	Aas07707 Cervical
C 422	23	1.3	288	4	AAH69821	Aah69821 Human cer
C 423	23	1.3	288	5	ADL43929	Adi43929 Human ova
C 424	23	1.3	289	4	AAH69822	Aah69822 Human cer
C 425	23	1.3	289	5	ADL43359	Adi43359 Human ova
C 426	23	1.3	289	5	ADI71439	Adi71439 Human ova
C 427	23	1.3	289	5	ADL36597	Adi36597 Human ova
C 428	23	1.3	289	14	ADY98877	Ady98877 T_reesei
C 429	23	1.3	290	5	ABV06729	Abv06729 Human pro
C 430	23	1.3	291	5	ABV37873	Abv37873 Human pro
C 431	23	1.3	292	5	ABV07826	Abv07826 Human pro
C 432	23	1.3	293	5	ADL72045	Adi72045 Human ova
C 433	23	1.3	293	5	ADL37194	Adi37194 Human ova
C 434	23	1.3	295	4	AA507819	Aas07819 Cervical
C 435	23	1.3	295	5	ADL38064	Adi38064 Human ova
C 436	23	1.3	295	5	ADI72927	Adi72927 Human ova
C 437	23	1.3	295	10	ABT22721	Abt22721 Breast ca
C 438	23	1.3	296	4	AA116259	Aal16259 Human bre
C 439	23	1.3	296	5	ADL36888	Adi36888 Human ova
C 440	23	1.3	296	5	ADL38330	Adi38330 Human ova
C 441	23	1.3	296	5	ADI71733	Adi71733 Human ova
C 442	23	1.3	296	5	ADI73198	Adi73198 Human ova
C 443	23	1.3	297	4	AA113342	Aal13342 Human bre
C 444	23	1.3	297	5	ABV06657	Abv06657 Human pro
C 445	23	1.3	297	5	ADL44514	Adi44514 Human ova
C 446	23	1.3	298	5	ABV38049	Abv38049 Human pro
C 447	23	1.3	298	5	ADI70275	Adi70275 Human ova
C 448	23	1.3	298	5	ADI76603	Adi76603 Human ova
C 449	23	1.3	299	5	ABV07684	Abv07684 Human pro
C 450	23	1.3	299	5	ADL36331	Adi36331 Human ova
C 451	23	1.3	299	5	ADI76880	Adi76880 Human ova
C 452	23	1.3	299	5	ADI70559	Adi70559 Human ova
C 453	23	1.3	299	5	ADI71171	Adi71171 Human ova
C 454	23	1.3	300	4	AAH69685	Aah69685 Human cer
C 455	23	1.3	300	5	ABV07828	Abv07828 Human pro
C 456	23	1.3	300	5	ADL37800	Adi37800 Human ova
C 457	23	1.3	300	5	ADL72661	Adi72661 Human ova
C 458	23	1.3	300	5	ADL38856	Adi38856 Human ova
C 459	23	1.3	301	5	ADI70712	Adi70712 Human ova
C 460	23	1.3	302	5	ABV07754	Abv07754 Human pro
C 461	23	1.3	303	4	AAH69954	Aah69954 Human cer
C 462	23	1.3	303	5	AAF98646	Aaf98646 Human ova
C 463	23	1.3	303	5	ADI71528	Adi71528 Human ova
C 464	23	1.3	303	5	ADL36684	Adi36684 Human ova
C 465	23	1.3	303	13	ACF84697	Acf84697 Human SIR
C 466	23	1.3	304	4	AA116023	Aal16023 Human bre
C 467	23	1.3	304	4	AAH69642	Aah69642 Human cer
C 468	23	1.3	304	5	ABV07365	Abv07365 Human pro
C 469	23	1.3	304	5	ABV37526	Abv37526 Human pro
C 470	23	1.3	304	5	ADL37322	Adi37322 Human ova
C 471	23	1.3	304	5	ADI72176	Adi72176 Human ova
C 472	23	1.3	305	4	AAH69979	Aah69979 Human cer
C 473	23	1.3	305	5	ADL36666	Adi36666 Human ova
C 474	23	1.3	305	5	ADI71510	Adi71510 Human ova
C 475	23	1.3	306	5	ABAI1166	Abai1166 Human ner
C 476	23	1.3	306	5	ABV37665	Abv37665 Human pro
C 477	23	1.3	307	4	AAH69658	Aah69658 Human cer
C 478	23	1.3	308	4	AA507748	Aas07748 Cervical
C 479	23	1.3	308	5	ADL36154	Adi36154 Human ova
C 480	23	1.3	308	5	ADI70991	Adi70991 Human ova
C 481	23	1.3	309	5	ADL37681	Adi37681 Human ova
C 482	23	1.3	309	5	ADI76735	Adi76735 Human ova
C 483	23	1.3	309	5	ADI72859	Adi72859 Human ova
C 484	23	1.3	309	5	ADL37998	Adi37998 Human ova
C 485	23	1.3	309	5	ADI70410	Adi70410 Human ova
C 486	23	1.3	309	5	ADL43267	Adi43267 Human ova
C 487	23	1.3	309	5	ADI72542	Adi72542 Human ova
C 488	23	1.3	310	4	AA507753	Aas07753 Cervical
C 489	23	1.3	310	5	AAF98609	Aaf98609 Human ova
C 490	23	1.3	311	14	ADY98689	Ady98689 T_reesei
C 491	23	1.3	312	4	AA114602	Aal14602 Human bre
C 492	23	1.3	312	4	AAH69906	Aah69906 Human cer
C 493	23	1.3	313	5	ADL44508	Adi44508 Human ova
C 494	23	1.3	313	5	ADL38460	Adi38460 Human ova
C 495	23	1.3	313	5	ADI73329	Adi73329 Human ova
C 496	23	1.3	314	5	ABV05899	Abv05899 Human pro
C 497	23	1.3	314	5	ADL38439	Adi38439 Human ova
C 498	23	1.3	314	5	ADL43941	Adi43941 Human ova
C 499	23	1.3	314	5	ADI73308	Adi73308 Human ova
C 500	23	1.3	314	10	ABT22928	Abt22928 Breast ca

ALIGNMENTS

RESULT 1

ABT13390

ID ABT13390 standard; DNA; 1713 BP.

XX

AC ABT13390;

XX

DT 30-JAN-2003 (first entry)

XX

DE Breast specific related polynucleotide SEQ ID No 105.

XX

KW Cytostatic; BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer;

KW metastatic; breast cancer; breast specific; human; ds.

XX

OS Homo sapiens.

FN WO200277232-A2.

XX

PD 03-OCT-2002.

XX

PF 21-NOV-2001; 2001WO-US043815.

XX

PR 22-NOV-2000; 2000US-0252509P.

XX

PA (DIAD-) DIADEXUS INC.

XX

ID	ADD01260 standard; cDNA; 2392 BP.	Matches 1695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX	ADD01260;	
AC		
XX		
DT	01-JAN-2004 (first entry)	
XX		
DE	Human nucleic acid-associated protein NAAP-41 cDNA SEQ ID NO:98.	
XX		
XX	human; nucleic acid-associated protein; NAAP; cytosolic;	
KW	antiarteriosclerotic; anti-HIV; anti-allergic; cerebroprotective;	
KW	anti-parkinsonian; anticonvulsant; neurotropic; neuroprotective;	
KW	anti-inflammatory; ophthalmological; thyromimetic; antiarthritic;	
KW	hepatotropic; antibacterial; virucide; protozoacide; antiparasitic;	
KW	fungicide; gene therapy; cell proliferative disease; cancer;	
KW	atherosclerosis; hepatitis; neurological disorder; Parkinson's disease;	
KW	Alzheimer's disease; stroke; epilepsy; developmental disorder;	
KW	renal tubular acidosis; anaemia; glaucoma; hypothyroidism;	
KW	autoimmune disorder; inflammatory disorder; AIDS; allergy;	
KW	atopic dermatitis; arthritis; infection; gene; ss.	
OS	Homo sapiens.	
XX		
XX	WO2003054219-A2.	
PN		
XX		
XX	03-JUL-2003.	
XX		
XX	18-DEC-2002; 2002WO-US041115.	
PF		
XX		
PR	19-DEC-2001; 2001US-0343004P.	
PR	11-JAN-2002; 2002US-0347633P.	
PR	25-JAN-2002; 2002US-0351749P.	
PR	22-FEB-2002; 2002US-0359498P.	
XX		
XX	(INCY-) INCYTE GENOMICS INC.	
FA		
XX		
PI	Azimzai Y, Baughn MR, Becha SD, Borowsky ML, Burford N;	
PI	Elliot V, Emerling BM, Forsythe IJ, Gorvad AE, Griffin JA;	
PI	Kable AE, Khare R, Lal SY, Lee EA, Lee SY, Li JX, Marquis JP;	
PI	Rankumar J, Richardson TW, Sprague WW, Swarnakar A, Tang YT,	
PI	Chawla NK, Warren BA, Yue H;	
XX		
DR	WPI; 2003-559157/52.	
DR	P-PSDB; ADD01203.	
XX		
XX	New human nucleic acid-associated proteins (NAAP), useful for diagnosing,	
PT	treating and preventing diseases or conditions associated with the	
PT	aberrant NAAP expression, e.g. cancer, hepatitis, AIDS, atherosclerosis,	
PT	infections.	
XX		
PS	Claim 5; SEQ ID NO 98; 405pp; English.	
XX		
CC	The present invention describes human nucleic acid-associated proteins	
CC	designated NAAP-1 to NAAP-57. The human NAAPs have cytosolic,	
CC	antiarteriosclerotic, anti-HIV, anti-allergic, cerebroprotective,	
CC	anti-parkinsonian, anticonvulsant, neurotropic, neuroprotective,	
CC	anti-inflammatory, ophthalmological, thyromimetic, antiarthritic,	
CC	hepatotropic, antibacterial, virucide, protozoacide, antiparasitic and	
CC	fungicide activities, and can be used in gene therapy. The NAAP protein	
CC	and polynucleotide sequences can be used in diagnosing, treating and	
CC	preventing diseases or conditions associated with the decreased	
CC	expression or overexpression of NAAP, such as cell proliferative diseases	
CC	(e.g. cancer, atherosclerosis, hepatitis), neurological disorders	
CC	(Parkinson's disease, Alzheimer's disease, stroke, epilepsy),	
CC	developmental disorders (renal tubular acidosis, anaemia, glaucoma,	
CC	hypothyroidism), autoimmune/inflammatory disorders (AIDS, allergies,	
CC	atopic dermatitis, arthritis) and infections (e.g. bacterial, viral,	
CC	parasitic, protozoal, fungal). The present sequence encodes human NAAP-	
CC	41, from the present invention.	
XX		
SQ	Sequence 2392 BP; 471 A; 743 C; 674 G; 504 T; 0 U; 0 Other;	
Query Match	96.0%; Score 1645; DB 10; Length 2392;	
Best Local Similarity	99.9%; Pred. No. 0;	


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Qy 361 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAAATGGAGTGCCTCCAGCCCTGATCGT 420
Db 450 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAAATGGAGTGCCTCCAGCCCTGATCGT 509
Qy 421 GCACCCCCCAGCCGGCGGGATGGCCAGCGGGCTCAAGTCAACCATGGGCGAGAGCTTCAGC 480
Db 510 GCACCCCCCAGCCGGCGGGATGGCCAGCGCTCAAGTCAACCATGGGCGAGAGCTTCAGC 569
Qy 481 TACCCCGATGTTAAGCTCAAAAGGCATCCCTGTGTATCCCTACCGAGGGCCACCTCCCCA 540
Db 570 TACCCCGATGTTAAGCTCAAAAGGCATCCCTGTGTATCCCTACCGAGGGCCACCTCCCCA 629
Qy 541 GCCCTGATCGGAGCTCTGCTGCAAGGAGCCACTGGCCGATCCCCACCCCATCGACAC 600
Db 630 GCCCTGATCGGAGCTCTGCTGCAAGGAGCCACTGGCCGATCCCCACCCCATCGGACAC 689
Qy 601 AGCTTGCCCGACACCTTTGCCAGTAGTCTCTGCTGGCTCCGAGGAGTACTATTTCTTCCAT 660
Db 690 AGCTTGCCCGACACCTTTGCCAGTAGTCTCTGCTGGCTCCGAGGAGTACTATTTCTTCCAT 749
Qy 661 GAGTCGACCTGAGACTCTCCGGAGATGGGCGAGTGGCTCCATGTGAGCCGAGAAATGAT 720
Db 750 GAGTCGACCTGAGACTCTCCGGAGATGGGCGAGTGGCTCCATGTGAGCCGAGAAATGAT 809
Qy 721 GTGCTCATCTTCAAGAGCTCACAGAGCTGTTCAAGCGTACACAGATCGATGAGCTGCC 780
Db 810 GTGCTCATCTTCAAGAGCTCACAGAGCTGTTCAAGCGTACACAGATCGATGAGCTGCC 869
Qy 781 AAGTGCAATCAGACACTGTGTTCTCGAGAGACCAGTAAGATCTCGAGCTTATCAGC 840
Db 870 AAGTGCAATCAGACACTGTGTTCTCGAGAGACCAGTAAGATCTCGAGCTTATCAGC 929
Qy 841 AGCATACGCGAGGACTACCACTGATGAGCAGAGATGCTGAGGGCGCTGGTACGGCGC 900
Db 930 AGCATACGCGAGGACTACCACTGATGAGCAGAGATGCTGAGGGCGCTGGTACGGCGC 989
Qy 901 ATCATTGTCATTAGTACCGAAGAGCGTCTCGCCACACAGACTCGAGGGTCTGTTCA 960
Db 990 ATCATTGTCATTAGTACCGAAGAGCGTCTCGCCACACAGACTCGAGGGTCTGTTCA 1049
Qy 961 ACTCGGGCTGTGCCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGGC 1020
Db 1050 ACTCGGGCTGTGCCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGGC 1109
Qy 1021 TCAGGTCTCAGCAGGATGAGCTGACAGTCAGATCTCCAGGAGACGACTGCGAGATGCC 1080
Db 1110 TCAGGTCTCAGCAGGATGAGCTGACAGTCAGATCTCCAGGAGACGACTGCGAGATGCC 1169
Qy 1081 ATGCCCGGAAGCTGAGSCCTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC 1140
Db 1170 ATGCCCGGAAGCTGAGSCCTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC 1229
Qy 1141 TTCCAGGSCACCGACAGACTCGTTCGGGGGCACCCCTTGCTCCAGGTGTACTGCTAACCC 1200
Db 1230 TTCCAGGSCACCGACAGACTCGTTCGGGGGCACCCCTTGCTCCAGGTGTACTGCTAACCC 1289
Qy 1201 CTGCCAGGCCAGCTGCCACACCTTTCTGGGAGAGCATGGCTTACAGAATGAAGAGGG 1260
Db 1290 CTGCCAGGCCAGCTGCCACACCTTTCTGGGAGAGCATGGCTTACAGAATGAAGAGGG 1349
Qy 1261 GGACCGAGAACCTCTGTGGGAGAGCTTGAACCTGMAAGCACTGCCCCCTCTGGCTCCCTCC 1320
Db 1350 GGAACAGAACCTCTGTGGGAGAGCTTGAACCTGMAAGCACTGCCCCCTCTGGCTCCCTCC 1409
Qy 1321 TGCCTTGCTGACTGGGTCTCTGGACCATGTGCAATTTTCACTGGGCCATGGGATCTACATC 1380
Db 1410 TGCCTTGCTGACTGGGTCTCTGGACCATGTGCAATTTTCACTGGGCCATGGGATCTACATC 1469
Qy 1381 TCCTTGATCCCGAGCTGGTCTGATCCCTGCGAGGGCCCTTCTCTTCTGCTCATGGTCT 1440
Db 1470 TCCTTGATCCCGAGCTGGTCTGATCCCTGCGAGGGCCCTTCTCTTCTGCTCATGGTCT 1529
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Qy 1441 TCAGTGGCTGTATCATGGAAAGTAAGAGTTAGGCATTACCTTCTGGAGTGAACCCCTG 1500
Db 1530 TCAGTGGCTGTATCATGGAAAGTAAGAGTTAGGCATTACCTTCTGGAGTGAACCCCTG 1589
Qy 1501 ACTCCATCCCTTATGCCACCTTAACCAATCATATGCAAACTTCTCCCTCCCTGGGGTAAT 1560
Db 1590 ACTCCATCCCTTATGCCACCTTAACCAATCATATGCAAACTTCTCCCTCCCTGGGGTAAT 1649
Qy 1561 TCACAGTAAACAAAGCTTATCTTAATGTATTTGTTATGGGGGTGGGCGAGGCCCACT 1620
Db 1650 TCACAGTAAACAAAGCTTATCTTAATGTATTTGTTATGGGGGTGGGCGAGGCCCACT 1709
Qy 1621 CTATGTTATGTTAAGGAGTTGGTTCTGTTCTGGCTGATGTTCTGTATCTTAACATGAC 1680
Db 1710 CTATGTTATGTTAAGGAGTTGGTTCTGTTCTGGCTGATGTTCTGTATCTTAACATGAC 1769
Qy 1681 CACAGTTTGTAAAGTAC 1696
Db 1770 CACAGTTTGTAAAGTAC 1785

RESULT 4
ABX92075
ID ABX92075 standard; cDNA; 1977 BP.
XX AC ABX92075;
XX AC
XX DT 08-MAY-2003 (first entry)
XX DE Lung specific nucleic acid (LSNA) #117.
XX KW Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
XX KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
XX KW non-cancerous diseases of the lung; transgenic animal; gene; ss.
XX OS Homo sapiens.
XX PN WO200268633-A2.
XX PD 06-SEP-2002.
XX PF 21-NOV-2001; 2001WO-US043612.
XX PR 22-NOV-2000; 2000US-0252500P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;
XX WPI; 2002-713376/77.

New isolated human nucleic acid molecule and polypeptide, useful for
identifying, diagnosing, monitoring, staging, imaging and treating lung
cancer and non-cancerous diseases of the lung.

Claim 1; Page 266-267; 389pp; English.

The invention describes an isolated human nucleic acid (I) encoding any
of 120 10-1533 residue amino acid sequences (S1), given in the
specification, comprising any of 164 179-12421 base pair sequences (S2),
given in the specification. The methods and compositions of the present
invention are useful for identifying, diagnosing, monitoring, staging,
imaging and treating lung cancer and non-cancerous diseases of the lung.
They are also used for identifying lung tissue, monitoring and
identifying and/or designing antagonists of the polypeptide of the
invention, gene therapy, production of transgenic animals and production
of engineered lung tissue for treatment and research. This sequence
encodes a lung specific nucleic acid

SQ Sequence 1977 BP; 393 A; 631 C; 554 G; 399 T; 0 U; 0 Other;
Query Match 57.4%; Score 983; DB 6; Length 1977;
Best Local Similarity 99.9%; Pred. No. 0;
```


Matches 1103; Conservative 0; Mismatches 0; Indels 1; Gaps 1;			
Qy	598	CACAGCTGCCAGACCTTTGCCAGTAGTCTCTGGTCTCGAGGAGTACTATTCTTTC	657
Db	861	CACAGCTGCCAGACCTTTGCCAGTAGTCTCTGGTCTCGAGGAGTACTATTCTTTC	920
Qy	658	CATGAGTCGGACCTGGACCTGCCAGATGGCAGTGGCTCATGTCCAGCGGAGAAATT	717
Db	921	CATGAGTCGGACCTGGACCTGCCAGATGGCAGTGGCTCATGTCCAGCGGAGAAATT	980
Qy	718	GATGTGCTCATCTTCAAGAAGCTGCAGA-GCTGTTCAGCGGTACACACAGATCGATGAGCT	776
Db	981	GATGTGCTCATCTTCAAGAAGCTGCAGA-GCTGTTCAGCGGTACACACAGATCGATGAGCT	1040
Qy	777	GGCCAAAGTGCACATCAGACATCTGTTCTTGGAGAAAGCCAGTAGATCTCGGACCTTAT	836
Db	1041	GGCCAAAGTGCACATCAGACATCTGTTCTTGGAGAAAGCCAGTAGATCTCGGACCTTAT	1100
Qy	837	CAGCAGCATCAGCAGGACTACCACTCTGGATGAGCAGGATGCTGAGGCCCGCTGGTAGC	896
Db	1101	CAGCAGCATCAGCAGGACTACCACTCTGGATGAGCAGGATGCTGAGGCCCGCTGGTAGC	1160
Qy	897	CGGCATCATTCGATTTAGTACCCGAAAGCCGTCTGCCACACAGACCTCGGAGGTCG	956
Db	1161	CGGCATCATTCGATTTAGTACCCGAAAGCCGTCTGCCACACAGACCTCGGAGGTCG	1220
Qy	957	TTCAACTCGGGTGTGTCGCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGCT	1016
Db	1221	TTCAACTCGGGTGTGTCGCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGCT	1280
Qy	1017	GGGCTCAGGTTTCAGCCAGATGAGTGAAGTGCAGATCTCCAGGAGACGACTGCAGA	1076
Db	1281	GGGCTCAGGTTTCAGCCAGATGAGTGAAGTGCAGATCTCCAGGAGACGACTGCAGA	1340
Qy	1077	TGCCATCCCGGAGCTGAGSCCTTATGAGTCCAGGCTACCGAGTACCGAAGCCATGACTC	1136
Db	1341	TGCCATCCCGGAGCTGAGSCCTTATGAGTCCAGGCTACCGAGTACCGAAGCCATGACTC	1400
Qy	1137	ATCCTTCAGGGCACCGACACAGACTCGTGGGGGACCCCTTGCTCCAGGTGTACTGCTA	1196
Db	1401	ATCCTTCAGGGCACCGACACAGACTCGTGGGGGACCCCTTGCTCCAGGTGTACTGCTA	1460
Qy	1197	ACCCCTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGATGGCCCTACAGATGAAG	1256
Db	1461	ACCCCTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGATGGCCCTACAGATGAAG	1520
Qy	1257	AGGGGACAGGAACCCCTGTGGAGAGGCTTAGACCTGAAGCAGTGCCTCTGGCTC	1316
Db	1521	AGGGGACAGGAACCCCTGTGGAGAGGCTTAGACCTGAAGCAGTGCCTCTGGCTC	1580
Qy	1317	CTCCTGCTTGGCTGACTGGGTTCTTGACCATGTGCATTTTCACTGGGCCATGGGATCTA	1376
Db	1581	CTCCTGCTTGGCTGACTGGGTTCTTGACCATGTGCATTTTCACTGGGCCATGGGATCTA	1640
Qy	1377	CATCTCTTGCAATCCCAAGCTGGTCTGATCCCTGCGAGGCCCTTCTCTGCTCATG	1436
Db	1641	CATCTCTTGCAATCCCAAGCTGGTCTGATCCCTGCGAGGCCCTTCTCTGCTCATG	1700
Qy	1437	GTCTTCAGTGGCCGTGATCATGGAAGTAAGAGTTAGGCATTACCTTCTGGAGTGAAC	1496
Db	1701	GTCTTCAGTGGCCGTGATCATGGAAGTAAGAGTTAGGCATTACCTTCTGGAGTGAAC	1760
Qy	1497	CCTGACTCCATCCCTTATGCGACCCCTAAACCAATCATGCAAACTTCTCCCTCCCTGGGG	1556
Db	1761	CCTGACTCCATCCCTTATGCGACCCCTTAAACCAATCATGCAAACTTCTCCCTCCCTGGGG	1820
Qy	1557	TAAATTCAACAGTTAAAGAAGCTTATCTTAAATGATTGTATTTGGGGGGTGGGACGGCC	1616
Db	1821	TAAATTCAACAGTTAAAGAAGCTTATCTTAAATGATTGTATTTGGGGGGTGGGACGGCC	1880
Qy	1617	CACCTATGTTATGTTAAGGAGTTGGTCTGGTCTTGGCTGATGTTCTGTATCTTAAACA	1676
Db	1881	CACCTATGTTATGTTAAGGAGTTGGTCTGGTCTTGGCTGATGTTCTGTATCTTAAACA	1940

Qy	1677	TGACCACAGTTTGTAAAGTACCTCG	1700
Db	1941	TGACCACAGTTTGTAAAGTACCTCG	1964
RESULT 5			
ID	ABX92014	standard; cDNA; 1977 BP.	
AC	ABX92014;		
DT	08-MAY-2003	(first entry)	
XX	Lung specific nucleic acid (LSNA) #56.		
DE	Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;		
KW	cancer monitoring; cancer staging; cancer imaging; lung cancer;		
KW	non-cancerous diseases of the lung; transgenic animal; gene; ss.		
OS	Homo sapiens.		
XX	WO200268633-A2.		
PN	06-SEP-2002.		
PD	21-NOV-2001; 2001WO-US043612.		
XX	22-NOV-2000; 2000US-0252500P.		
PR	(DIAD-) DIADEXUS INC.		
XX	Macina RA, Recipon H, Chen S, Sun Y, Liu C;		
PI	WPI; 2002-713376/77.		
XX	New isolated human nucleic acid molecule and polypeptide, useful for		
DR	identifying, diagnosing, monitoring, staging, imaging and treating lung		
XX	cancer and non-cancerous diseases of the lung.		
PT	Claim 1; Page 205-206; 389pp; English.		
PT	The invention describes an isolated human nucleic acid (I) encoding any		
XX	of 120 10-1533 residue amino acid sequences (S1), given in the		
CC	specification, comprising any of 164 179-12421 base pair sequences (S2),		
CC	given in the specification. The methods and compositions of the present		
CC	invention are useful for identifying, diagnosing, monitoring, staging,		
CC	imaging and treating lung cancer and non-cancerous diseases of the lung.		
CC	They are also used for identifying lung tissue, monitoring and		
CC	identifying and/or designing antagonists of the polypeptide of the		
CC	invention, gene therapy, production of transgenic animals and production		
CC	of engineered lung tissue for treatment and research. This sequence		
CC	encodes a lung specific nucleic acid		
XX	Sequence 1977 BP; 393 A; 631 C; 554 G; 399 T; 0 U; 0 Other;		

Query Match 57.4%; Score 983; DB 6; Length 1977;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1103; Conservative 0; Mismatches 0; Indels 1; Gaps 1;			
Qy	598	CACAGCTGCCAGACCTTTGCCAGTAGTCTCTGGTCTCGAGGAGTACTATTCTTTC	657
Db	861	CACAGCTGCCAGACCTTTGCCAGTAGTCTCTGGTCTCGAGGAGTACTATTCTTTC	920
Qy	658	CATGAGTCGGACCTGGACCTGCCAGATGGCAGTGGCTCATGTCCAGCGGAGAAATT	717
Db	921	CATGAGTCGGACCTGGACCTGCCAGATGGCAGTGGCTCATGTCCAGCGGAGAAATT	980
Qy	718	GATGTGCTCATCTTCAAGAAGCTGCAGA-GCTGTTCAGCGGTACACACAGATCGATGAGCT	776
Db	981	GATGTGCTCATCTTCAAGAAGCTGCAGA-GCTGTTCAGCGGTACACACAGATCGATGAGCT	1040
Qy	777	GGCCAAAGTGCACATCAGACATCTGTTCTTGGAGAAAGCCAGTAGATCTCGGACCTTAT	836

Db 1041 GGCACAGTGCATCAGACACTGTGTTCTCTGGAGAAGACCAAGTAGAATCTCGGACCTTAT 1100
Qy 837 CAGCAGCATCAGCAGGACTACCACTGGATGAGCAGATGCTGAGGCCGCCCTGGTACG 896
Db 1101 CAGCAGCATCAGCAGGACTACCACTGGATGAGCAGATGCTGAGGCCGCCCTGGTACG 1160
Qy 897 CGGCATCATTCGCATTAGTACCGAAGAGCGGTGCTCGCCACACAGACTCGGAGGGTCG 956
Db 1161 CGGCATCATTCGCATTAGTACCGAAGAGCGGTGCTCGCCACACAGACTCGGAGGGTCG 1220
Qy 957 TTCAACTCGGCTGCTGCCCCAACCGCTGTGCCCCGTGACAGTGGCCCATGAGACCATGGT 1016
Db 1221 TTCAACTCGGCTGCTGCCCCAACCGCTGTGCCCCGTGACAGTGGCCCATGAGACCATGGT 1280
Qy 1017 GGGCTCAGGCTCAGCAGATGAGCTGACAGTGCAGATCTCCAGGAGCAGCTGCAGA 1076
Db 1281 GGGCTCAGGCTCAGCAGATGAGCTGACAGTGCAGATCTCCAGGAGCAGCTGCAGA 1340
Qy 1077 TGCCATCGCCCGAAGCTGAGGCCCTTATGGAGCTCCAGGGTACCAGCAAGCCATGACTC 1136
Db 1341 TGCCATCGCCCGAAGCTGAGGCCCTTATGGAGCTCCAGGGTACCAGCAAGCCATGACTC 1400
Qy 1137 ATCCTTCCAGGGCACCGACACAGACTCGTGGGGGACCCCTTGCTCCAGGTGTACTGCTA 1196
Db 1401 ATCCTTCCAGGGCACCGACACAGACTCGTGGGGGACCCCTTGCTCCAGGTGTACTGCTA 1460
Qy 1197 ACCCTGCGCCGCGAGCTGACACACACTTCTGGGAGAACATGGCTCAGCAATGAAG 1256
Db 1461 ACCCTGCGCCGCGAGCTGACACACACTTCTGGGAGAACATGGCTCAGCAATGAAG 1520
Qy 1257 AGGGGGACAGAAACCCCTGTGGAGAGGCTTAGACCTGAAGAGTGCCCACTCTGGCTC 1316
Db 1521 AGGGGGACAGAAACCCCTGTGGAGAGGCTTAGACCTGAAGAGTGCCCACTCTGGCTC 1580
Qy 1317 CTCCTGCTTGGCTGACTGGGTTCTTGACCATGTGCAATTTCACTGGGCCCATGGGATCTA 1376
Db 1581 CTCCTGCTTGGCTGACTGGGTTCTTGACCATGTGCAATTTCACTGGGCCCATGGGATCTA 1640
Qy 1377 CATCTCTTGATCCCGAGCTGGTCTGATCCTGTCAGGGGCCCTTCCTCTGCTCATG 1436
Db 1641 CATCTCTTGATCCCGAGCTGGTCTGATCCTGTCAGGGGCCCTTCCTCTGCTCATG 1700
Qy 1437 GTCTTCAGTGGCTGATCATGGAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAAC 1496
Db 1701 GTCTTCAGTGGCTGATCATGGAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAAC 1760
Qy 1497 CCTGACTCCATPCCCCCTATTGCCACCCCTAACCAATCATGCAAACTTCTCCCTCGGG 1556
Db 1761 CCTGACTCCATPCCCCCTATTGCCACCCCTAACCAATCATGCAAACTTCTCCCTCGGG 1820
Qy 1557 TAATTCACAGTTAAAGAACCTTATCTTAATGATTTGATGGGGGTGGGAGGGCC 1616
Db 1821 TAATTCACAGTTAAAGAACCTTATCTTAATGATTTGATGGGGGTGGGAGGGCC 1880
Qy 1617 CACTCTATGTTATGTTAAGGAGTTGGTCTCGTCTGGCTGATGTTCTGATCTTAACA 1676
Db 1881 CACTCTATGTTATGTTAAGGAGTTGGTCTCGTCTGGCTGATGTTCTGATCTTAACA 1940
Qy 1677 TGACCACAGTTTGTAAAGTACCTCG 1700
Db 1941 TGACCACAGTTTGTAAAGTACCTCG 1964

RESULT 6
ID AEA19545
AC AEA19545 standard; cDNA; 791 BP.
XX AC AEA19545;
XX DT 11-AUG-2005 (first entry)
XX DE Novel human polynucleotide SEQ ID NO 239.

XX vulnery; CNS-gen.; gene therapy; diagnostic; forensic; mapping;
KW DNA purification; protein purification; osteoarthritis; antiarthritic;
KW osteopathic; musculoskeletal disease; osteoporosis; endocrine disease;
KW periodontal disease; antiinflammatory; mouth disease; burns; injury;
KW peripheral neuropathy; Alzheimers disease; neuroprotective; neurotropic;
KW degeneration; parkinsons disease; antiparkinsonian; neurological disease;
KW cerebrovascular ischemia; cerebroprotective; vasotropic;
KW cardiovascular disease; autoimmune disease; immunosuppressive;
KW immune disorder; viral infection; virucide; infection; cancer;
KW cystostatic; neoplasm; gene; ss.
XX Homo sapiens.
XX WO2005049806-A2.
XX 02-JUN-2005.
XX 11-MAR-2004; 2004WO-US007412.
XX 14-MAR-2003; 2003US-00389559.
XX (NUVE-) NUVELO INC.
XX Tang TY, Wang J, Wang ZW, Zhang J, Ren F, Zhou P, Ma Y;
PI Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R;
PI Wehrman T, Weng G, Boyle B;
XX MPI; 2005-417730/42.
DR P-PSDB; AEA20112.
XX New polynucleotide encoding a polypeptide with biological activity,
PT useful for treating a disease or disorder, e.g. osteoarthritis, burns,
PT CNS and peripheral disease, stroke, autoimmune disorders, viral
PT infection, or cancer.
XX Claim 1; SEQ ID NO 239; 500pp; English.
XX The invention describes a new isolated polynucleotide (I) encoding a
CC polypeptide with biological activity comprising: a nucleotide sequence of
CC SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes
CC to the sequence of (i) under stringent hybridization conditions; or a
CC nucleotide sequence having greater than 9% sequence identity with the
CC sequence of (i). Also described are: a(n) (expression) vector comprising
CC (I); a host cell genetically engineered to comprise (I) operatively,
CC associated with a regulatory sequence that modulates expression of the
CC polynucleotide in the host cell; an isolated polypeptide comprising a
CC sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide
CC is: a polypeptide encoded by (I); or a polypeptide encoded by a
CC polynucleotide hybridizing under stringent conditions with any one of SEQ
CC ID NOS: 1-567; a composition comprising the polypeptide of (3) and a
CC carrier; an antibody directed against the polypeptide of (3); a method
CC for detecting (I) in a sample; a method for identifying a compound that binds to the
CC (3) in a sample; a method for producing the polypeptide of (3); and a
CC collection of polynucleotides, where the collection comprising of at
CC least one of SEQ ID NOS: 1-567, (I) is a polynucleotide comprising any of
CC the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological
CC activity, which comprises any of the amino acid sequence of SEQ ID NOS:
CC 568-1134. All sequences are fully defined in the specification. The
CC sequences and methods are useful in diagnostics, forensic, and gene
CC mapping, in identifying of mutations responsible for genetic disorders or
CC other traits, in assessing biodiversity, and for producing many other
CC types of data and products dependent on DNA and amino acid sequences. The
CC composition and method are useful for treating a disease or disorder,
CC e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and
CC peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,
CC autoimmune disorders, viral infection, or cancer. This sequence encodes a
CC novel polypeptide of the invention.
XX Sequence 791 BP; 149 A; 278 C; 222 G; 142 T; 0 U; 0 Other;
SQ

Query Match 39.9%; Score 683; DB 14; Length 791;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 CAACAGAGCTATGCTGGAGACATATGATAAACCACTCAGCCCCCACCACCAAGCCGCGCA 124
DB 64 CAACAGAGCTATGCTGGAGACATATGATAAACCACTCAGCCCCCACCACCAAGCCGCGCA 123
QY 125 CCGGTAGACACACCCCAAGGACCTTGGCCACATGAGGCGCAGAGCATTACCTTCATCT 184
DB 124 CCGGTAGACACACCCCAAGGACCTTGGCCACATGAGGCGCAGAGCATTACCTTCATCT 183
QY 185 CTGGCTCTGCTCAGCGCGCCCTTGAGTCCCCACCTGCTGCTCTGCGGCGCAGCCCTGGG 244
DB 184 CTGGCTCTGCTCAGCGCGCCCTTGAGTCCCCACCTGCTGCTCTGCGGCGCAGCCCTGGG 243
QY 245 TGTGGAGTGTGCCGGCTGCTTCTGCTTCCGCGCTGCGCGGATTCCTCCAGCGCT 304
DB 244 TGTGGAGTGTGCCGGCTGCTTCTGCTTCCGCGCTGCGCGGATTCCTCCAGCGCT 303
QY 305 GTGGAGCTGTGTGGGGATGAGCCCTGCTGTCTACTAGGACTCCACTGAGGGGA 364
DB 304 GTGGAGCTGTGTGGGGATGAGCCCTGCTGTCTACTAGGACTCCACTGAGGGGA 363
QY 365 CTGCTGAAGCAACTGGGCCAAGGAGCAATGGAGTGCCCCCAGCCCTGATCGTCAC 424
DB 364 CTGCTGAAGCAACTGGGCCAAGGAGCAATGGAGTGCCCCCAGCCCTGATCGTCAC 423
QY 425 CCCCCAGCGCGGATGCCAGCGGCTCAAGTCAACCATGGCGCAGCAGCTTCAGCTACC 484
DB 424 CCCCCAGCGCGGATGCCAGCGGCTCAAGTCAACCATGGCGCAGCAGCTTCAGCTACC 483
QY 485 CCGATGTTAAGCTCAAGGATCCCTGTGTATCCCTTACCCGAGGCGCAGCTCCCGAGGCC 544
DB 484 CCGATGTTAAGCTCAAGGATCCCTGTGTATCCCTTACCCGAGGCGCAGCTCCCGAGGCC 543
QY 545 CTGATGCGGACTCTGCTGCAAGGAGCCACTGGCGGATCCCCCAGCCATGGACACAGCC 604
DB 544 CTGATGCGGACTCTGCTGCAAGGAGCCACTGGCGGATCCCCCAGCCATGGACACAGCC 603
QY 605 TGCCCCAGCACCTTTGCCAGTAGTCTCTGCTGCTCCGAGGAGTACTATTCTTCCATGAGT 664
DB 604 TGCCCCAGCACCTTTGCCAGTAGTCTCTGCTGCTCCGAGGAGTACTATTCTTCCATGAGT 663
QY 665 CGGACTGGACCTGCGGAGATGGGAGTGGCTCCATGTGCGAGCGAGAAATTGATGTC 724
DB 664 CGGACTGGACCTGCGGAGATGGGAGTGGCTCCATGTGCGAGCGAGAAATTGATGTC 723
QY 725 TCATCTTCAAGAGCTGACAGAG 747
DB 724 TCATCTTCAAGAGCTGACAGAG 746

RESULT 7
ABX92013
ID ABX92013 standard; cDNA; 385 BP.
XX AC ABX92013;
XX DT 08-MAY-2003 (first entry)
XX XX Lung specific nucleic acid (LSNA) #55.
DE Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
KW non-cancerous diseases of the lung; transgenic animal; gene; ss.
XX Homo sapiens.
OS
XX WO200268633-A2.
XX PN
XX PD 06-SEP-2002.
XX PF 21-NOV-2001; 2001WO-US043612.

XX 22-NOV-2000; 2000US-0252500P.
XX (DIAD-) DIADEXUS INC.
XX Macina RA, Recipon H, Chen S, Sun Y, Liu C;
XX WPI; 2002-713376/77.
XX New isolated human nucleic acid molecule and polypeptide, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating lung
PT cancer and non-cancerous diseases of the lung.
XX Claim 1; Page 204-205; 389pp; English.
XX The invention describes an isolated human nucleic acid (I) encoding any
CC of 120 10-1533 residue amino acid sequences (S1), given in the
CC specification, comprising any of 164 179-12421 base pair sequences (S2),
CC given in the specification. The methods and compositions of the present
CC invention are useful for identifying, diagnosing, monitoring, staging,
CC imaging and treating lung cancer and non-cancerous diseases of the lung.
CC They are also used for identifying lung tissue, monitoring and
CC identifying and/or designing antagonists of the polypeptide of the
CC invention, gene therapy, production of transgenic animals and production
CC of engineered lung tissue for treatment and research. This sequence
CC encodes a lung specific nucleic acid
XX
SQ Sequence 385 BP; 80 A; 122 C; 93 G; 90 T; 0 U; 0 Other;
Query Match 22.5%; Score 385; DB 6; Length 385;
Best Local Similarity 100.0%; Pred. No. 3.5e-174;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 ACTGTAACCCCTGCGAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGGCCCTACAG 1249
DB 1 ACTGTAACCCCTGCGAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGGCCCTACAG 60
QY 1250 AATGAAGAGGGGAGCAGGAACCCCTGTGGGAGAGCTTAGACCTGAAGCAGTGGCCACT 1309
DB 61 AATGAAGAGGGGAGCAGGAACCCCTGTGGGAGAGCTTAGACCTGAAGCAGTGGCCACT 120
QY 1310 CTGGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1369
DB 121 CTGGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 1370 GGATCTACATCTCTTGTGATCCCGAGCTGGTCTGATCCCTGCGAGGCCCTTCTCTTCT 1429
DB 181 GGATCTACATCTCTTGTGATCCCGAGCTGGTCTGATCCCTGCGAGGCCCTTCTCTTCT 240
QY 1430 GCTCATGCTTCTCAGGTGGCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGG 1489
DB 241 GCTCATGCTTCTCAGGTGGCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGG 300
QY 1490 AGTGAACCTGACTCCATCCCGCTTATGGCACCCTAACCAATCATGCAGAACTTCTCCCTC 1549
DB 301 AGTGAACCTGACTCCATCCCGCTTATGGCACCCTAACCAATCATGCAGAACTTCTCCCTC 360
QY 1550 CTGGGGTAATTCACAGTTAAAG 1574
DB 361 CTGGGGTAATTCACAGTTAAAG 385

RESULT 8
ABT07644
ID ABT07644 standard; cDNA; 386 BP.
XX AC ABT07644;
XX DT 14-NOV-2002 (first entry)
XX XX Human breast cancer associated coding sequence SEQ ID NO: 123.
DE Human; breast specific gene; breast specific protein; breast cancer;
KW


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RESULT 10
AAAF64421
ID   AAF64421 standard; cDNA; 393 BP.
XX
AC   AAF64421;
XX
DT   09-APR-2001 (first entry)
XX
DE   Novel human polynucleotide, SEQ ID NO: 177.
XX
KW   Human; cytostatic; gene therapy; colon cancer; prostate cancer;
KW   breast cancer; lung cancer; cancer detection; ss.
XX
OS   Homo sapiens.
XX
PN   WO200102568-A2.
XX
PD   11-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US018374.
XX
PR   02-JUL-1999; 99US-0142310P.
PR   02-JUL-1999; 99US-0142311P.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J;
PI   Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G;
PI   Drmanac R, Crkenjakov R, Drmanac S, Dickson M, Labat I;
PI   Leshkowitz D, Kita D, Garcia V, Jones LW, Strache-Crain B;
XX
DR   WPI; 2001-091805/10.
XX
PT   Library of polynucleotides for diagnosing a cancerous state of a
PT   mammalian cell and detecting cancer, particularly of the colon or
PT   prostate, comprises 3351 human polynucleotide sequences.
XX
PS   Claim 9; Page 570; 1046pp; English.
XX
CC   The present sequence is one of 3351 sequences in a library of human
CC   polynucleotides. The library is used to detect differentially expressed
CC   genes correlated with a cancerous state of a mammalian cell and can
CC   detect colon, prostate, breast and lung cancer. The library can be used
CC   to produce probes for detection of mRNA and to produce additional copies
CC   of the polynucleotides. The probes can be used for chromosome mapping of
CC   the polynucleotide and for detection of transcription levels. Ribozymes
CC   or antisense oligonucleotides can be generated. The polynucleotides and
CC   their gene products are used as genetic or biochemical markers (e.g. in
CC   blood or tissues) that will detect the earliest changes along the
CC   carcinogenesis pathway and/or monitor the efficacy of therapies and
CC   preventive interventions. The polynucleotides, polypeptides and
CC   antibodies against them can be used in pharmaceutical compositions to
CC   treat the cancers and proliferative disorders such as neoplasia,
CC   dysplasia and hyperplasia
XX
SQ   Sequence 393 BP; 88 A; 122 C; 115 G; 67 T; 0 U; 1 Other;
Query Match      19.5%; Score 334; DB 5; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.1e-149;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 805 CTGAGAGAGACAGTAAGATCTCGGACCTTATCAGCAGCATCACGAGACTTACCACCTG 864
DB 21 CTGGAGAGACAGTAAGATCTCGGACCTTATCAGCAGCATCACGAGACTTACCACCTG 80
QY 865 GATGAGCAGGATGCTGAGGGCGCGCTGTGATCGCGGCATCTTCGATTAGTACCCGAAG 924
DB 81 GATGAGCAGGATGCTGAGGGCGCGCTGTGATCGCGGCATCTTCGATTAGTACCCGAAG 140
QY 925 AGCCGTGTCGCCACACAGCTTCGGGGTGTTCACCTCGGGTGTGCCACCGCT 984
DB 141 AGCCGTGTCGCCACACAGCTTCGGGGTGTTCACCTCGGGTGTGCCACCGCT 200
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QY 985 GCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGTCTCAGCCAGGATGAGCTG 1044
DB 201 GCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGTCTCAGCCAGGATGAGCTG 260
QY 1045 ACAGTGCAGATCTCCAGGAGACGACTGCAGATGCATCGCCGGAAGCTGAGGCTTAT 1104
DB 261 ACAGTGCAGATCTCCAGGAGACGACTGCAGATGCATCGCCGGAAGCTGAGGCTTAT 320
QY 1105 GGAGTCCAGGTTACCCAGCAAGCCATGACTCAT 1138
DB 321 GGAGTCCAGGTTACCCAGCAAGCCATGACTCAT 354

RESULT 11
AAAF66376
ID   AAF66376 standard; cDNA; 427 BP.
XX
AC   AAF66376;
XX
DT   09-APR-2001 (first entry)
XX
DE   Novel human polynucleotide, SEQ ID NO: 2132.
XX
KW   Human; cytostatic; gene therapy; colon cancer; prostate cancer;
KW   breast cancer; lung cancer; cancer detection; ss.
XX
OS   Homo sapiens.
XX
PN   WO200102568-A2.
XX
PD   11-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US018374.
XX
PR   02-JUL-1999; 99US-0142310P.
PR   02-JUL-1999; 99US-0142311P.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J;
PI   Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G;
PI   Drmanac R, Crkenjakov R, Drmanac S, Dickson M, Labat I;
PI   Leshkowitz D, Kita D, Garcia V, Jones LW, Strache-Crain B;
XX
DR   WPI; 2001-091805/10.
XX
PT   Library of polynucleotides for diagnosing a cancerous state of a
PT   mammalian cell and detecting cancer, particularly of the colon or
PT   prostate, comprises 3351 human polynucleotide sequences.
XX
PS   Claim 9; Page 854; 1046pp; English.
XX
CC   The present sequence is one of 3351 sequences in a library of human
CC   polynucleotides. The library is used to detect differentially expressed
CC   genes correlated with a cancerous state of a mammalian cell and can
CC   detect colon, prostate, breast and lung cancer. The library can be used
CC   to produce probes for detection of mRNA and to produce additional copies
CC   of the polynucleotides. The probes can be used for chromosome mapping of
CC   the polynucleotide and for detection of transcription levels. Ribozymes
CC   or antisense oligonucleotides can be generated. The polynucleotides and
CC   their gene products are used as genetic or biochemical markers (e.g. in
CC   blood or tissues) that will detect the earliest changes along the
CC   carcinogenesis pathway and/or monitor the efficacy of therapies and
CC   preventive interventions. The polynucleotides, polypeptides and
CC   antibodies against them can be used in pharmaceutical compositions to
CC   treat the cancers and proliferative disorders such as neoplasia,
CC   dysplasia and hyperplasia
XX
SQ   Sequence 427 BP; 69 A; 161 C; 123 G; 73 T; 0 U; 1 Other;
Query Match      18.7%; Score 321; DB 5; Length 427;
```

Best Local Similarity 100.0%; Pred. No. 2e-143;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCCCGCCCTTGACACCCCGCCAGCATCTGGGCTCCACCGTTGGGACCGTGGAG 60
Db 80 ATGCCCGCCCTTGACACCCCGCCAGCATCTGGGCTCCACCGTTGGGACCGTGGAG 139
Qy 61 CGGCCAACAGAGCTATGCTGGAGACATATGATATTAACCACTCAGCCGCCACCAAGCGC 120
Db 140 CGGCCAACAGAGCTATGCTGGAGACATATGATATTAACCACTCAGCCGCCACCAAGCGC 199
Qy 121 CGCACCCGTAGACAGACCCCAAGACCCCTGGCCACCATGGGCCAGAGACATTACCTTC 180
Db 200 CGCACCCGTAGACAGACCCCAAGACCCCTGGCCACCATGGGCCAGAGACATTACCTTC 259
Qy 181 ATCTCTGGCTCTGCTAGCCGGCCCTTGAGTCCGCCACCTGCTGCTCTGCTGGGACCC 240
Db 260 ATCTCTGGCTCTGCTAGCCGGCCCTTGAGTCCGCCACCTGCTGCTCTGCTGGGACCC 319
Qy 241 TGGGTGTGGAGTGTGCGGGCTGCTTCTGCTTCCGCCGCTGCGGGATTGCTCCAG 300
Db 320 TGGGTGTGGAGTGTGCGGGCTGCTTCTGCTTCCGCCGCTGCGGGATTGCTCCAG 379
Qy 301 CGCTGTGGAGCCTGTGTGCGG 321
Db 380 CGCTGTGGAGCCTGTGTGCGG 400

RESULT 12
AAZ13392
ID AAZ13392 standard; cDNA; 300 BP.
XX AC AAZ13392;
XX DT 12-OCT-1999 (first entry)
XX DE Human gene expression product cDNA sequence SEQ ID NO:861.
XX KW Human; gene; gene expression product; diagnosis; therapy; probe;
KW detection; mapping; tissue typing; profiling; forensic; cancer;
KW genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX OS Homo sapiens.
XX DN WO9938972-A2.
XX PD 05-AUG-1999.
XX PF 28-JAN-1999; 99WO-US001619.
XX PR 28-JAN-1998; 98US-0072910P.
PR 24-FEB-1998; 98US-0075954P.
PR 31-MAR-1998; 98US-0080114P.
PR 03-APR-1998; 98US-0080515P.
PR 03-APR-1998; 98US-0080666P.
PR 21-OCT-1998; 98US-0105234P.
PR 28-OCT-1998; 98US-0105877P.
XX (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX WPI; 1999-494092/41.
XX Novel human genes and their expression products which are differentially
PT expressed in different cell types.
XX Claim 1; Page 860; 2479pp; English.
XX

The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ17779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists

Seq Sequence 300 BP; 63 A; 96 C; 90 G; 51 T; 0 U; 0 Other;
Query Match 17.5%; Score 300; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 825 CTCGGACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGG 884
Db 1 CTCGGACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGG 60
Qy 885 CCGCTGTACGGCGCATCTCGCATTTAGTACCCGAAAGAGCCGCTGCGCCACAGAC 944
Db 61 CCGCTGTACGGCGCATCTCGCATTTAGTACCCGAAAGAGCCGCTGCGCCACAGAC 120
Qy 945 CTCGGAGGGTCTTTCAACTCGGGCTGCTGCCCAACCGCTGCTCCCTGACAGTGCCA 1004
Db 121 CTCGGAGGGTCTTTCAACTCGGGCTGCTGCCCAACCGCTGCTCCCTGACAGTGCCA 180
Qy 1005 TGAGACCATGGTGGCTTCAGGCTTCAGCCAGGATGAGCTGACAGTGAGATCTCCAGGA 1084
Db 181 TGAGACCATGGTGGCTTCAGGCTTCAGCCAGGATGAGCTGACAGTGAGATCTCCAGGA 240
Qy 1065 GACGACTGCAGATGCCATCGCCGAGAGCTTATGGAGCTCCAGGATACCCAGC 1124
Db 241 GACGACTGCAGATGCCATCGCCGAGAGCTTATGGAGCTCCAGGATACCCAGC 300

RESULT 13
AAZ98308
ID AAZ98308 standard; cDNA; 300 BP.
XX AC AAZ98308;
XX DT 24-SEP-1999 (first entry)
XX DE Human cancer cell derived cDNA #34.
XX Cancer; human; colon; breast; lung; transmembrane receptor; ATPase;
KW integral membrane protein; aspartyl protease; GATA family; wnt family;
KW transcription factor; G-protein alpha subunit; protein phosphatase;
KW phospholipase binding protein; diacylglycerol binding protein; trypsin;
KW protein kinase; tyrosine phosphatase; developmental signalling protein;
KW WW/rps5/WWP domain; therapy; forensic; genetic mapping; diagnostic;
KW detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
KW Wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
KW leukemia; lymphoma; dysplasia; hyperplasia; endometrium; adrenal;
KW prostate; ss.
XX OS Homo sapiens.
XX Claim 1; Page 860; 2479pp; English.
XX

XX PD 08-JUL-1999.
XX PF 22-DEC-1998; 98WO-US027610.
XX PR 23-DEC-1997; 97US-0068755P.
XX PR 03-APR-1998; 98US-0080664P.
XX PR 21-OCT-1998; 98US-0105234P.
XX PR 27-OCT-1998; 98US-0105877P.
XX PR 21-DEC-1998; 98US-00217471.
XX PA (CHIR) CHIRON CORP.
XX PA (HYSE-) HYSEQ INC.
XX PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
XX WPI; 1999-430243/36.
XX DR New isolated human polynucleotides.
XX PT Claim 1; Page 326; 591pp; English.
XX PS This invention describes novel isolated human polynucleotides obtained by
CC screening for differential expression in colon cancer, breast cancer and
CC lung cancer cell lines. The polynucleotides of the invention are
CC represented in AAX98275-X99118 and encode polypeptides of protein
CC families selected from 4 transmembrane segments integral membrane
CC proteins, 7 transmembrane receptors, Arafases associated with various
CC cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
CC transcription factors, G-protein alpha subunit, phospholipase or
CC diacylglycerol binding proteins, protein kinase, protein phosphatase 2C,
CC protein tyrosine phosphatase, tryptase, wnt family of developmental
CC signalling proteins and WW/rsp5/WWP domain containing proteins. The
CC encoded polypeptides also have a functional domain selected from Ank
CC repeat, basic region plus leucine zipper transcription factors,
CC bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger
CC (C2H2 type), zinc finger (CCHC class), and zinc-binding metalloprotease
CC domain. The polynucleotides encode polypeptides with similarity to known
CC protein families and are predicted to have similar properties. The novel
CC polynucleotides can be used to develop products for use as therapeutic
CC agents and in forensics, genetic analysis, mapping and diagnostic
CC applications. In particular, the product can be used for the detection
CC and management of cancers. They can be used for treating e.g. cervical
CC cancers, melanomas, colorectal adenocarcinomas, Wilm's tumour, sarcomas,
CC retinoblastoma, myosarcomas, lung carcinomas, leukemias, such as chronic
CC myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and
CC myeloid leukemia, and lymphomas such as histiocytic lymphoma, anhydric
CC hereditary ectodermal dysplasia, congenital alveolar dysplasia,
CC epithelial dysplasia of the cervix, fibrous dysplasia of bone, and
CC mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
CC prostate or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of
CC the skin
XX SQ Sequence 300 BP; 68 A; 90 C; 86 G; 56 T; 0 U; 0 Other;

Query Match 14.5%; Score 249; DB 2; Length 300;
Best Local Similarity 99.7%; Pred. No. 7.9e-109;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGACAGAGCTGTTTCAGCGGTACACACAGATCGATGAGCTGGCCCAAGTGACATCAGACACTG 799
DB 1 TGACAGAGCTGTTTCAGCGGTACACACAGATCGATGAGCTGGCCCAAGTGACATCAGACACTG 60

QY 800 TGTTCCTGAGAGAACCAAGTAGATTCGGACCTTTATCAGCAGCATACGCGAGGACTACC 859
DB 61 TGTTCCTGAGAGAACCAAGTAGATTCGGACCTTTATCAGCAGCATACGCGAGGACTACC 120

QY 860 ACCTGGATGAGCAGATGCTGAGGGCCGCTGGTACGGGGCATCATTCGCATTAGTACC 919
DB 121 ACCTGGATGAGCAGATGCTGAGGGCCGCTGGTACGGGGCATCATTCGCATTAGTACC 180

QY 920 GAAAGAGCCGTGCTCGGCCCAACAGACCTCGGAGGGTGGTTCAACTCGGGCTGCTGCCCCAA 979
DB 181 GAAAGAGCCGTGCTCGGCCCAACAGACCTCGGAGGGTGGTTCAACTCGGGCTGCTGCCCCAA 240

QY 980 CCGCTGCTGCCCTGAGCAGTGGCCATGAGACCATGTTGGGCTCAGGTTCTCAGCCAGGATG 1039
DB 241 CCGCTGCTGCCCTGAGCAGTGGCCATGAGACCATGTTGGGCTCAGGTTCTCAGCCAGGATG 300

RESULT 14
ABT07645
ID ABT07645 standard; cDNA; 654 BP.
XX AC
XX ABT07645;
XX AC
XX 14-NOV-2002 (first entry)
XX DT
XX Human breast cancer associated coding sequence SEQ ID NO: 124.
XX DE
XX Human; breast specific gene; breast specific protein; breast cancer;
XX KW gene therapy; cytostatic; gene; ss.
XX KW
XX Homo sapiens.
XX OS
XX WO200264611-A1.
XX PN
XX 22-AUG-2002.
XX PD
XX 12-FEB-2002; 2002WO-US004197.
XX PF
XX 13-FEB-2001; 2001US-0268292P.
XX PR
XX (DIAD-) DIADEXUS INC.
XX PA
XX Salceda S, Macina RA, Hu P, Recipon H, Karra K, Cafferkey R;
XX PI Sun Y, Liu C;
XX WPI; 2002-657582/70.
XX DR
XX New breast specific nucleic acids and proteins, useful for identifying,
XX PT diagnosing, monitoring, staging, imaging, and treating breast cancer and
XX PT non-cancerous disease states in breast tissue, and in gene therapy.
XX PS Claim 1; Page 248; 367pp; English.
XX CC The present invention provides human breast specific coding sequences and
XX CC proteins. These can be used in the diagnosis and treatment of breast
XX CC cancer and non-cancerous diseases of the breast. The present sequence is
XX CC a coding sequence of the invention
XX SQ Sequence 654 BP; 118 A; 232 C; 186 G; 118 T; 0 U; 0 Other;

Query Match 13.0%; Score 222; DB 6; Length 654;
Best Local Similarity 100.0%; Pred. No. 7.4e-96;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 ATGATAAACCACTCAGCCCCCAGAGCCGCGCCAGCCGCTAGACACAGACCCCAAGGACC 148
DB 1 ATGATAAACCACTCAGCCCCCAGAGCCGCGCCAGCCGCTAGACACAGACCCCAAGGACC 60

QY 149 CTGGCCACCATGGGCCAGAGAGCATTAACCTTTCATCTCTGGCTCTGCTGAGCGGCGCTTG 208
DB 61 CTGGCCACCATGGGCCAGAGAGCATTAACCTTTCATCTCTGGCTCTGCTGAGCGGCGCTTG 120

QY 209 AGTCCCCCAGCTGCTGCTGCTCTGGGACCCCTGGGTGTGGAGTGGTGGCGGCTGCT 268
DB 121 AGTCCCCCAGCTGCTGCTGCTCTGGGACCCCTGGGTGTGGAGTGGTGGCGGCTGCT 180

QY 269 TCTGCTTCGCGCGCTGCGGGATTGCTTCCAGCGCTGTGGAG 310
DB 181 TCTGCTTCGCGCGCTGCGGGATTGCTTCCAGCGCTGTGGAG 222


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AA117411
ID AAL17411 standard; cDNA; 576 BP.
XX
AC AAL17411;
XX
XX 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 9868.
XX
KW Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.
XX
XX 10-JAN-2001; 2001WO-US000799.
XX
PF 14-JAN-2000; 2000US-0176077P.
PR 14-MAR-2000; 2000US-0189167P.
PR 24-MAR-2000; 2000US-0192099P.
PR 29-MAR-2000; 2000US-0193480P.
PR 15-MAY-2000; 2000US-0205230P.
PR 09-JUN-2000; 2000US-0211313P.
PR 25-JUL-2000; 2000US-0220534P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX
XX WPI; 2001-451856/48.
XX
DR New peptide useful as a marker for the diagnosis of breast cancer.
XX
PS Claim 1; Page 1758; 3695pp; English.
XX
CC The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AA126789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity
XX
SQ Sequence 576 BP; 134 A; 111 C; 125 G; 205 T; 0 U; 1 Other;
Query Match 1.5%; Score 26; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1688 TGTAGTACTCGCGCGGACCAACGC 1713
DB 550 TGTAGTACTCGCGCGGACCAACGC 575
RESULT 23
ABZ08482
ID ABZ08482 standard; cDNA; 224 BP.
XX
AC ABZ08482;
XX
XX 09-JAN-2003 (first entry)
XX
DE Human leukocyte derived cDNA SEQ ID NO 8473.
XX
KW Human; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; gene;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
XX 22-OCT-2001; 2001WO-US047856.
XX
XX 20-OCT-2000; 2000US-0241994P.
PR 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quertermous T, Johnson F;
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 26; Page 1920; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ0010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection. The
XX present sequence is that of a human leukocyte expressed cDNA of the
XX invention
XX
SQ Sequence 224 BP; 80 A; 44 C; 44 G; 44 T; 0 U; 12 Other;
Query Match 1.5%; Score 25; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1689 GTAAGTACTCGCGCGGACCAACGC 1713
DB 189 GTAAGTACTCGCGCGGACCAACGC 213
RESULT 24
ABV37465/c
ID ABV37465 standard; cDNA; 255 BP.
XX
AC ABV37465;
XX
XX 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 37456.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
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PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 7689; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the efficacy
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 255 BP; 56 A; 55 C; 80 G; 64 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 25; DB 5; Length 255;
XX Best Local Similarity 100.0%; Pred. No. 0.34;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1689 GTAAGTACTCGCGCGACACGC 1713
XX |||||||
XX Db 97 GTAAGTACTCGCGCGACACGC 73
XX
XX RESULT 25
XX ADL43520/c
XX ID ADL43520 standard; DNA; 275 BP.
XX
XX AC ADL43520;
XX
XX XX 20-MAY-2004 (first entry)
XX
XX Human ovarian cancer DNA marker #17410.
XX
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
XX Homo sapiens.
XX
XX WO200170979-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
XX
XX 25-MAY-2000; 2000US-0207124P.
XX
XX 15-JUN-2000; 2000US-0211940P.
XX
XX 07-JUL-2000; 2000US-0216820P.
XX
XX 25-JUL-2000; 2000US-0220661P.
XX
XX 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX
XX WPI; 2001-611502/70.
XX
XX 25-MAY-2000; 2000US-0207454P.
XX
XX 09-JUN-2000; 2000US-0211314P.
XX
XX 18-JUL-2000; 2000US-0219007P.
XX
XX 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 7689; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the efficacy
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 255 BP; 56 A; 55 C; 80 G; 64 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 25; DB 5; Length 255;
XX Best Local Similarity 100.0%; Pred. No. 0.34;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1689 GTAAGTACTCGCGCGACACGC 1713
XX |||||||
XX Db 97 GTAAGTACTCGCGCGACACGC 73
XX
XX RESULT 26
XX ABV07533/c
XX ID ABV07533 standard; cDNA; 304 BP.
XX
XX AC ABV07533;
XX
XX XX 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 7524.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX
XX 17-FEB-2000; 2000US-0183319P.
XX
XX 16-MAR-2000; 2000US-0189862P.
XX
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PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 1214; 11750pp; English.
PS
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 304 BP; 80 A; 63 C; 78 G; 76 T; 0 U; 7 Other;
SQ
Query Match 1.5%; Score 25; DB 5; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1689 GTAAGTACTCGCGCGACACCGC 1713
|||||
Db 39 GTAAGTACTCGCGCGACACCGC 15
|||||
RESULT 27
ADL37497
ID ADL37497 standard; DNA; 310 BP.
XX AC
XX ADL37497;
XX
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #11387.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX DR

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 11387; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 310 BP; 91 A; 72 C; 73 G; 74 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 25; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1689 GTAAGTACTCGCGCGACACCGC 1713
|||||
Db 280 GTAAGTACTCGCGCGACACCGC 304
|||||
RESULT 28
ADI72353
ID ADI72353 standard; DNA; 310 BP.
XX AC
XX ADI72353;
XX
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #5095.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009126.
XX
XX 21-MAR-2000; 2000US-0191031P.

PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
DR
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
XX
PS Disclosure; SEQ ID NO 5095; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 310 BP; 91 A; 72 C; 73 G; 74 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1689 GTAAGTACCTCGCGCGACACGC 1713
Db 280 GTAAGTACCTCGCGCGACACGC 304
RESULT 29
AAL14408/c
ID AAL14408 standard; cDNA; 358 BP.
XX
XX AAL14408;
XX
XX 07-DEC-2001 (first entry)
DI Human breast cancer expressed polynucleotide 6865.
DE
XX

KW Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX WO200151628-A2.
XX
XX 19-JUL-2001.
XX
XX 10-JAN-2001; 2001WO-US000798.
XX
XX 14-JAN-2000; 2000US-0176077P.
PR 14-MAR-2000; 2000US-0189167P.
PR 24-MAR-2000; 2000US-0192099P.
PR 29-MAR-2000; 2000US-0193480P.
PR 15-MAY-2000; 2000US-0205230P.
PR 09-JUN-2000; 2000US-0211315P.
PR 25-JUL-2000; 2000US-0220534P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2001-451856/48.
DR
XX New peptide useful as a marker for the diagnosis of breast cancer.
PT
XX Claim 1; Page 1239; 3695pp; English.
XX
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity
XX
SQ Sequence 358 BP; 105 A; 60 C; 81 G; 102 T; 0 U; 10 Other;
Query Match 1.5%; Score 25; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1689 GTAAGTACCTCGCGCGACACGC 1713
Db 31 GTAAGTACCTCGCGCGACACGC 7
RESULT 30
AAH69711/c
ID AAH69711 standard; cDNA; 359 BP.
XX
XX AAH69711;
XX
XX 19-SEP-2001 (first entry)
DI Human cervical cancer marker nucleic acid 985.
DE
XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX Homo sapiens.
XX WO200142467-A2.
XX
XX 14-JUN-2001.
XX
XX 08-DEC-2000; 2000WO-US033312.
XX
XX 08-DEC-1999; 99US-0169681P.
PR 21-DEC-1999; 99US-0171350P.
PR 14-MAR-2000; 2000US-0189315P.
PR 12-MAY-2000; 2000US-0203791P.


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PR 09-JUN-2000; 2000US-0210600P.
XX 21-JUL-2000; 2000US-0220114P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Deeds J, Berger A, Zhao X;
XX WPI; 2001-375006/39.
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
XX for assessing and detecting compounds for treating the cancer.
XX Claim 1; Page 264; 1051pp; English.
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
XX cervical cancer with cytostatic activity. The nucleic acids and encoded
XX polypeptides are useful: to assess if a patient is afflicted with
XX cervical cancer or has a pre-malignant condition; to monitor the
XX progression of cervical cancer or a premalignant condition in a patient;
XX and to select and/or assess the efficacy of a compound or therapy for
XX inhibiting cervical cancer in a patient. The nucleic acids may also be
XX useful for gene therapy
XX
XX Sequence 359 BP; 92 A; 57 C; 74 G; 135 T; 0 U; 1 Other;
SQ
Query Match 1.5%; Score 25; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1689 GTAAGTACTCGCGCGGACCCACGC 1713
DB 31 GTAAGTACTCGCGCGGACCCACGC 7
RESULT 31
ABV98985
ID ABV98985 standard; cDNA; 453 BP.
XX
AC ABV98985;
XX
XX 14-JAN-2003 (first entry)
XX Human pancreatic cancer expressed cDNA SEQ ID NO 4393.
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
XX cytostatic; tumour; gene; ss.
XX Homo sapiens.
XX WO200260317-A2.
XX
XX 08-AUG-2002.
XX
XX 30-JAN-2002; 2002WO-US002781.
XX
XX 30-JAN-2001; 2001US-0265305P.
XX 31-JAN-2001; 2001US-0265682P.
XX 09-FEB-2001; 2001US-0267568P.
XX 21-MAR-2001; 2001US-0278651P.
XX 28-APR-2001; 2001US-0287112P.
XX 16-MAY-2001; 2001US-0291631P.
XX 12-JUL-2001; 2001US-0305484P.
XX 20-AUG-2001; 2001US-0313999P.
XX 27-NOV-2001; 2001US-0333626P.
XX (CORI-) CORIYA CORP.
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX WPI; 2002-627435/67.
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
XX diagnosing, preventing and/or treating cancer, particularly pancreatic
PT
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PT cancer.
XX Claim 1; SEQ ID NO 4393; 300pp + Sequence Listing; English.
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
XX any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
XX complements of (a); (c) sequences consisting of at least 20 contiguous
XX residues of (a); (d) sequences that hybridize to (a), under moderately
XX stringent conditions; (e) sequences having at least 75% or 90% identity
XX to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
XX ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
XX in a patient and compositions comprising polypeptides, polynucleotides,
XX antibodies, fusion proteins, T cell populations and antigen presenting
XX cells expressing the polypeptide are useful in treating pancreatic cancer
XX and stimulating an immune response. The polynucleotides can be used as
XX probes or primers for nucleic acid hybridisation, in the design and
XX preparation of ribozyme molecules for inhibiting expression of the tumour
XX polypeptides and proteins in the tumour cells, in vaccines and for gene
XX therapy. Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 453 BP; 100 A; 93 C; 131 G; 129 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 25; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1689 GTAAGTACTCGCGCGGACCCACGC 1713
DB 428 GTAAGTACTCGCGCGGACCCACGC 452
RESULT 32
ADL43881
ID ADL43881 standard; DNA; 463 BP.
XX
AC ADL43881;
XX
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #17771.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 17771; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
XX
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ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 463 BP; 123 A; 110 C; 117 G; 113 T; 0 U; 0 Other;

Query Match 1.5%; Score 25; DB 5; Length 463;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAAGTACCTCGCGCGACACGC 1713

Db 351 GTAAGTACCTCGCGCGACACGC 375

RESULT 33

ABS67274/C
ID ABS67274 standard; cDNA; 810 BP.

XX AC ABS67274;

XX DT 29-NOV-2002 (first entry)

XX DE Breast specific polynucleotide #10.

XX KW Breast specific; cancer staging; cancer imaging; breast cancer;
XX KW non-cancerous disease states in breast tissue; gene therapy; vaccine;
XX KW transgenic animal; gene; ss.

XX OS Homo sapiens.

XX PN WO200264741-A2.

XX PD 22-AUG-2002.

XX PF 12-FEB-2002; 2002WO-US004134.

XX PR 13-FEB-2001; 2001US-0268289P.

XX PA (DIAD-) DIADEXUS INC.

XX PI Salceda S, Macina RA, Hu P, Recipon H, Karra K, Cafferkey R;
XX PI Liu C, Sun Y;

DR WPI; 2002-657590/70.

XX PT New breast specific nucleic acids and proteins, for identifying,
PT diagnosing, monitoring, staging, imaging, and treating breast cancer and
PT non-cancerous disease states in breast tissue, or for gene therapy.

XX Claim 1; Page 156; 227pp; English.

XX CC The invention describes a breast specific nucleic acid. The nucleic
CC acids, polypeptides, antibodies, agonists and antagonists, and
CC compositions comprising them are useful for identifying, diagnosing,
CC monitoring, staging, imaging, and treating breast cancer and non-
CC cancerous disease states in breast tissue, in gene therapy, vaccine
CC development, in producing transgenic animals and cells, and in producing
CC engineered breast tissue for treatment and research. The nucleic acids
CC may be used as molecular markers for detecting breast cancer for accurate
CC staging of the disease and monitoring the progress of cancer treatments,
CC and as hybridisation probes or primers. This sequence encodes a breast
CC specific protein of the invention

SQ Sequence 810 BP; 216 A; 183 C; 145 G; 266 T; 0 U; 0 Other;

Query Match 1.5%; Score 25; DB 6; Length 810;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAAGTACCTCGCGCGACACGC 1713

Db 25 GTAAGTACCTCGCGCGACACGC 1

RESULT 34

ACN84455/C

ID ACN84455 standard; DNA; 1252 BP.

XX AC ACN84455;

XX DT 02-DEC-2004 (first entry)

XX DE Breast cancer related marker, seq id 5605.

XX KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.

XX OS Homo sapiens.

XX PN US2003099974-A1.

XX PD 29-MAY-2003.

XX PF 18-JUL-2002; 2002US-00198846.

XX PR 18-JUL-2001; 2001US-0306220P.

XX PA (MTLL-) MILLENNIUM PHARM INC.

XX PI Lillie J, Xu Y, Wang Y, Steinmann K;

XX DR WPI; 2003-787014/74.

XX PT Novel isolated polypeptide associated with breast cancer, useful for
PT detecting presence of polypeptide in sample, as a marker for breast
PT cancer.

XX PS Disclosure; SEQ ID NO 5605; 36pp; English.

XX CC The invention relates to an isolated polypeptide (I) associated with
CC breast cancer which is encoded by a nucleic acid molecule comprising a
CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
CC the polypeptide of the invention. The activity of the polypeptide of the
CC invention may be described as cytostatic. The antibody is useful for
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC invention are useful in the detection of breast tumours. (I) is useful as
CC a marker for breast cancer and in breast cancer therapy. Sequences given

CC in records ACN78851-ACN92934 represent nucleic acid markers associated
CC with breast cancer. Note: The sequence listing does not form part of the
CC specification but may be obtained in electronic format from the USPTO web
CC site at seqdata.uspto.gov/sequence.html?DocID=20030099974

XX Sequence 1252 BP; 269 A; 229 C; 238 G; 336 T; 0 U; 180 Other;

Query Match 1.5%; Score 25; DB 11; Length 1252;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACCTCGCGCGACACGC 1713

Db 224 GTAAGTACCTCGCGCGACACGC 200

RESULT 35

ADY99697/c

ID ADY99697 standard; cDNA; 150 BP.

XX AC ADY99697;

XX 16-JUN-2005 (first entry)

DE T_reesei suppressive subtractive hybridization (SSH) cDNA clone Seq 1051.

XX gene expression; suppressive subtractive hybridization; microarray;
KW microorganism; ss.

XX Hypocrea jecorina.

XX US2005069934-A1.

XX 31-MAR-2005.

XX 24-SEP-2004; 2004US-00950009.

XX 25-SEP-2003; 2003US-0506140P.

XX (NOVO) NOVOZYMES BIOTECH INC.

XX Berk A, Bashkirtova E, Rey M;

XX WPI; 2005-271963/28.

XX Monitoring differential expression of genes of two filamentous fungal
XX cells, for e.g. discovering new genes, comprises adding labeled nucleic
XX acids to an array of Trichoderma reesei expressed sequenced tags and
XX detecting spots.

PS Claim 1; SEQ ID NO 1051; 27pp; English.

XX This invention relates to a novel method for monitoring differential
XX expression of genes in a filamentous fungal cell. Specifically, it refers
XX to identifying differential gene expression occurring between two related
XX filamentous fungal cells and comprises adding detection reporter labeled
XX nucleic acids of filamentous fungal cells to a substrate array of
XX Trichoderma reesei (T. reesei) expressed sequenced tags (ESTs), or
XX suppression subtractive hybridization (SSH) clones and detecting a signal
XX in the array. The present invention further describes a computer readable
XX medium having for monitoring differential expression of several genes in
XX a first filamentous fungal cell relative to expression of the same genes
XX in one or more second filamentous fungal cells. It also provides a search
XX unit for comparing a target sequence to a T. reesei EST sequence of the
XX data storage unit to identify homologous sequences, and a retrieval unit
XX for obtaining the homologous sequence(s). Accordingly, it provides a
XX method useful for identifying microbial genes induced when the
XX microorganism is grown on cellulose or corn stover, as well as for
XX discovering new genes, identifying possible functions of unknown open
XX reading frames and monitoring gene copy number variation and stability.
XX Note that this method utilizes an array where one spot equals one gene or
XX open reading frame, which makes extensive follow-up characterization
XX unnecessary since sequence information is available and EST and/or SSH

CC microarrays can be organized based on function of the gene products. This
CC polynucleotide sequence is a T. reesei SSH cDNA clone that forms part of
CC the substrate array of the invention. NOTE: The SeqIDs 1-1188 referring
CC to T. reesei ESTs or SSH clones or their combinations are available in
CC electronic form from the USPTO web site
CC (<http://seqdata.uspto.gov/sequence.html>; Document ID:20050069934).

XX Sequence 150 BP; 35 A; 38 C; 42 G; 35 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 14; Length 150;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713

Db 24 TAAGTACCTCGCGCGACACGC 1

RESULT 36

ABT23431

ID ABT23431 standard; DNA; 232 BP.

XX AC ABT23431;

XX 08-MAY-2003 (first entry)

DE Immune-related mouse DNA SEQ ID No 15.

XX Antiallergic; antiinflammatory; antiasthmatic; dermatological;
KW ophthalmological; immunosuppressive; immune related; allergic;
KW autoimmune; inflammatory; infectious disease; asthma; allergic rhinitis;
KW atopic dermatitis; hives; conjunctivitis; systemic lupus erythematosus;
KW myasthenia gravis; psoriasis; sepsis; gout; colitis; immunisation;
KW gene therapy; mouse; murine; da.

XX Mus musculus.

XX WO2003002599-A2.

XX 09-JAN-2003.

XX 10-MAY-2002; 2002WO-EP005127.

XX 11-MAY-2001; 2001US-0290312P.

XX (FARB) BAYER AG.

XX Encinas J, Leong J;

XX WPI; 2003-210241/20.

XX New polynucleotide encoding a protein with biological properties of a
XX human immune-related protein, useful for treating diseases related to
XX immune-related protein, e.g. allergic, inflammatory, autoimmune or
XX infectious diseases.

PS Claim 1; Fig 15; 180pp; English.

XX The invention relates to an isolated polynucleotide which encodes an
XX immune related protein or a protein exhibiting biological properties of
XX an immune-related protein with a sequence selected from 26 sequences. The
XX expression vector and reagent are useful for the preparation of a
XX medicament for modulating the activity of a human immune-related protein
XX in a disease, such as allergic, autoimmune, inflammatory or infectious
XX diseases, e.g. asthma, allergic rhinitis, atopic dermatitis, hives,
XX conjunctivitis, systemic lupus erythematosus, myasthenia gravis,
XX psoriasis, sepsis, gout, or colitis. The polypeptides may also be used to
XX identify compounds which may act as activators or inhibitors at the
XX enzyme's active site, to raise specific antibodies which can block the
XX enzyme and effectively reduce its activity, as a bait protein in a two-
XX hybrid or three-hybrid assay to identify other proteins which bind to or
XX interact with the human immune-related protein and modulate its activity,
XX and for immunisation of mammals. The polynucleotides of the invention can

CC be used in gene therapy for treating disorders. This sequence represents
CC an immune-related mouse protein of the invention. This polynucleotide
CC represents an immune-related mouse DNA sequence of the invention

XX Sequence 232 BP; 52 A; 43 C; 49 G; 86 T; 0 U; 2 Other;

Query Match 1.4%; Score 24; DB 8; Length 232;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1698 TGTAAGTACCTCGCGCGGACAC 1711
|||||
Db 207 TGTAAGTACCTCGCGCGGACAC 230
|||||

RESULT 37
ADL43332/c
ID ADL43332 standard; DNA; 253 BP.
XX
AC ADL43332;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #17222.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
FN WO200170979-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lee J, Lillie J;
XX
DR WPI; 2001-611502/70.
XX

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 17222; 106pp; English.

PS The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the

CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

SQ Sequence 253 BP; 44 A; 65 C; 65 G; 79 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
|||||
Db 77 TAAGTACCTCGCGCGGACACGC 54
|||||

RESULT 38
ADL37742/c
ID ADL37742 standard; DNA; 274 BP.
XX
AC ADL37742;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #11632.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
FN WO200170979-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lee J, Lillie J;
XX
DR WPI; 2001-611502/70.
XX

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 11632; 106pp; English.

PS The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted

CC with ovarian cancer, which involves comparing the level of expression of
 CC a marker in a patient sample and a normal level of expression of the
 CC marker in a control non-ovarian cancer sample. A difference between the
 CC expression levels indicates ovarian cancer. The level of expression of a
 CC marker corresponds to a secreted protein or to a transcribed
 CC polynucleotide or its portion. The level of expression of the marker is
 CC assessed by detecting the presence in the sample, a protein or protein
 CC fragment corresponding to the marker. The presence of protein or protein
 CC fragment is detected using an antibody that specifically binds with the
 CC protein or protein fragment. Alternatively, the level of expression of
 CC the marker is assessed by detecting the presence of a transcribed
 CC polynucleotide which anneals with the marker or anneals with a portion of
 CC the polynucleotide comprising the marker, under stringent conditions. The
 CC marker is also used for monitoring the progression of ovarian cancer in a
 CC patient which involves detecting expression of the marker in a patient
 CC sample at a first point in time, repeating the method at a subsequent
 CC time and comparing the level of expression. The method is carried out
 CC using an ovarian tissue sample. A composition comprising a marker,
 CC polypeptide or antibody of the invention is used to treat ovarian cancer.
 CC This sequence represents a human ovarian cancer DNA marker of the
 CC invention.

SQ Sequence 274 BP; 79 A; 63 C; 63 G; 69 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 274;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCTCGCGCGACGACGC 1713
 Db 30 TAAGTACTCTCGCGCGACGACGC 7

RESULT 39
 ADI72603/c
 ID ADI72603 standard; DNA; 274 BP.
 XX
 AC ADI72603;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human ovarian cancer DNA marker #5345.
 XX
 KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
 XX
 OS Homo sapiens.
 XX
 FN WO200170979-A2.
 XX
 PD 27-SEP-2001.
 XX
 XX 21-MAR-2001; 2001WO-US009126.
 XX
 XX 21-MAR-2000; 2000US-0191031P.
 PR 25-MAY-2000; 2000US-0207124P.
 PR 15-JUN-2000; 2000US-0211940P.
 PR 07-JUL-2000; 2000US-0216820P.
 PR 25-JUL-2000; 2000US-0220661P.
 PR 21-DEC-2000; 2000US-0257672P.
 XX

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Lee J, Lillie J;

WPI; 2001-611502/70.

Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
 PT cancer cells as compared to their normal non-cancerous ovarian cells are
 PT used to characterize stage, grade, histological type of ovarian cancer.

PS Disclosure; SEQ ID NO 5345; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in

CC ovarian cancer cells as compared to their expression in normal (i.e. non-
 CC cancerous) ovarian cells. The invention also relates to polypeptides
 CC encoded by the markers, antibodies that selectively bind to the
 CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
 CC of developing ovarian cancer involving inhibiting expression of a gene
 CC corresponding to a marker of the invention and a method of treating a
 CC patient afflicted with ovarian cancer comprising providing to cells of
 CC the patient an antisense oligonucleotide complementary to a marker of the
 CC invention. The markers are useful for assessing if a patient is afflicted
 CC with ovarian cancer, which involves comparing the level of expression of
 CC a marker in a patient sample and a normal level of expression of the
 CC marker in a control non-ovarian cancer sample. A difference between the
 CC expression levels indicates ovarian cancer. The level of expression of a
 CC marker corresponds to a secreted protein or to a transcribed
 CC polynucleotide or its portion. The level of expression of the marker is
 CC assessed by detecting the presence in the sample, a protein or protein
 CC fragment corresponding to the marker. The presence of protein or protein
 CC fragment is detected using an antibody that specifically binds with the
 CC protein or protein fragment. Alternatively, the level of expression of
 CC the marker is assessed by detecting the presence of a transcribed
 CC polynucleotide which anneals with the marker or anneals with a portion of
 CC the polynucleotide comprising the marker, under stringent conditions. The
 CC marker is also used for monitoring the progression of ovarian cancer in a
 CC patient which involves detecting expression of the marker in a patient
 CC sample at a first point in time, repeating the method at a subsequent
 CC time and comparing the level of expression. The method is carried out
 CC using an ovarian tissue sample. A composition comprising a marker,
 CC polypeptide or antibody of the invention is used to treat ovarian cancer.
 CC This sequence represents a human ovarian cancer DNA marker of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 274 BP; 79 A; 63 C; 63 G; 69 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 274;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCTCGCGCGACGACGC 1713
 Db 30 TAAGTACTCTCGCGCGACGACGC 7

RESULT 40
 ADL42505/c
 ID ADL42505 standard; DNA; 283 BP.
 XX
 AC ADL42505;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human ovarian cancer DNA marker #16395.
 XX
 KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
 XX
 OS Homo sapiens.
 XX
 FN WO200170979-A2.
 XX
 PD 27-SEP-2001.
 XX
 XX 21-MAR-2001; 2001WO-US009126.
 XX
 XX 21-MAR-2000; 2000US-0191031P.
 PR 25-MAY-2000; 2000US-0207124P.
 PR 15-JUN-2000; 2000US-0211940P.
 PR 07-JUL-2000; 2000US-0216820P.
 PR 25-JUL-2000; 2000US-0220661P.
 PR 21-DEC-2000; 2000US-0257672P.
 XX

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX

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PI Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 16395; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 283 BP; 94 A; 62 C; 50 G; 77 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 283;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1690 TAAGTACTCTCGCGCGGACACGCG 1713
XX Db 54 TAAGTACTCTCGCGCGGACACGCG 31
XX
XX RESULT 41
XX ADI70936/c
XX ID ADI70936 standard; DNA; 310 BP.
XX
XX AC ADI70936;
XX
XX XX 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #3678.
XX
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX OS Homo sapiens.
XX FN WO200170979-A2.
XX PD 27-SEP-2001.
XX DE Human ovarian cancer DNA marker #9991.
XX
XX 21-MAR-2001; 2001WO-US009126.
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 3678; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 310 BP; 72 A; 54 C; 66 G; 118 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 310;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1690 TAAGTACTCTCGCGCGGACACGCG 1713
XX Db 30 TAAGTACTCTCGCGCGGACACGCG 7
XX
XX RESULT 42
XX ADI77249/c
XX ID ADI77249 standard; DNA; 310 BP.
XX
XX AC ADI77249;
XX
XX XX 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #9991.
XX
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XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
KW Homo sapiens.
OS WO200170979-A2.
XX 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009126.
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
PT
PS Disclosure; SEQ ID NO 9991; 106pp; English.
XX
CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 310 BP; 72 A; 54 C; 66 G; 118 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCGCGCGGACCGC 1713
|||||
DB 30 TAAGTACTCGCGCGGACCGC 7

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 312 BP; 99 A; 53 C; 47 G; 113 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCGCGCGGACACGC 1713
|||||
DB 30 TAAGTACTCGCGCGGACACGC 7

RESULT 45
ADI71332/C
ID ADI71332 standard; DNA; 312 BP.
XX
AC ADI71332;
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #4074.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009126.
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 4074; 106pp; English.
XX
CC The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the

CC polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention.
XX
SQ Sequence 312 BP; 99 A; 53 C; 47 G; 113 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCGCGCGGACACGC 1713
|||||
DB 30 TAAGTACTCGCGCGGACACGC 7

RESULT 45
ADI70234/C
ID ADI70234 standard; DNA; 319 BP.
XX
AC ADI70234;
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #2976.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009126.
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 2976; 106pp; English.
XX
CC The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the

CC marker in a control non-ovarian cancer sample. A difference between the
 CC expression levels indicates ovarian cancer. The level of expression of a
 CC marker corresponds to a secreted protein or to a transcribed
 CC polynucleotide or its portion. The level of expression of the marker is
 CC assessed by detecting the presence in the sample, a protein or protein
 CC fragment corresponding to the marker. The presence of protein or protein
 CC fragment is detected using an antibody that specifically binds with the
 CC protein or protein fragment. Alternatively, the level of expression of
 CC the marker is assessed by detecting the presence of a transcribed
 CC polynucleotide which anneals with the marker or anneals with a portion of
 CC the polynucleotide comprising the marker, under stringent conditions. The
 CC marker is also used for monitoring the progression of ovarian cancer in a
 CC patient which involves detecting expression of the marker in a patient
 CC sample at a first point in time, repeating the method at a subsequent
 CC time and comparing the level of expression. The method is carried out
 CC using an ovarian tissue sample. A composition comprising a marker,
 CC polypeptide or antibody of the invention is used to treat ovarian cancer.
 CC This sequence represents a human ovarian cancer DNA marker of the
 CC invention.

XX
 SQ Sequence 319 BP; 77 A; 61 C; 78 G; 99 T; 0 U; 4 Other;
 Query Match 1.4%; Score 24; DB 5; Length 319;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACCTCGCGCGACACGC 1713
 |||||
 Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 46
 ADI76563/c
 ID ADI76563 standard; DNA; 319 BP.
 XX
 AC ADI76563;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human ovarian cancer DNA marker #9305.
 XX
 KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
 XX
 OS Homo sapiens.
 XX
 PN WO200170979-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US009126.
 XX
 PR 21-MAR-2000; 2000US-0191031P.
 PR 25-MAY-2000; 2000US-0207124P.
 PR 15-JUN-2000; 2000US-0211940P.
 PR 07-JUL-2000; 2000US-0216820P.
 PR 25-JUL-2000; 2000US-0220661P.
 PR 21-DEC-2000; 2000US-0257672P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Lee J, Lillie J;
 XX
 DR WPI; 2001-611502/70.
 XX
 PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
 PT cancer cells as compared to their normal non-cancerous ovarian cells are
 PT used to characterize stage, grade, histological type of ovarian cancer.
 XX
 PS Disclosure; SEQ ID NO 9305; 106pp; English.
 XX
 CC The invention relates to nucleic acid markers which are overexpressed in
 CC ovarian cancer cells as compared to their expression in normal (i.e. non-
 CC cancerous) ovarian cells. The invention also relates to polypeptides

CC encoded by the markers, antibodies that selectively bind to the
 CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
 CC of developing ovarian cancer involving inhibiting expression of a gene
 CC corresponding to a marker of the invention and a method of treating a
 CC patient afflicted with ovarian cancer comprising providing to cells of
 CC the patient an antisense oligonucleotide complementary to a marker of the
 CC invention. The markers are useful for assessing if a patient is afflicted
 CC with ovarian cancer, which involves comparing the level of expression of
 CC a marker in a patient sample and a normal level of expression of the
 CC marker in a control non-ovarian cancer sample. A difference between the
 CC expression levels indicates ovarian cancer. The level of expression of a
 CC marker corresponds to a secreted protein or to a transcribed
 CC polynucleotide or its portion. The level of expression of the marker is
 CC assessed by detecting the presence in the sample, a protein or protein
 CC fragment corresponding to the marker. The presence of protein or protein
 CC fragment is detected using an antibody that specifically binds with the
 CC protein or protein fragment. Alternatively, the level of expression of
 CC the marker is assessed by detecting the presence of a transcribed
 CC polynucleotide which anneals with the marker or anneals with a portion of
 CC the polynucleotide comprising the marker, under stringent conditions. The
 CC marker is also used for monitoring the progression of ovarian cancer in a
 CC patient which involves detecting expression of the marker in a patient
 CC sample at a first point in time, repeating the method at a subsequent
 CC time and comparing the level of expression. The method is carried out
 CC using an ovarian tissue sample. A composition comprising a marker,
 CC polypeptide or antibody of the invention is used to treat ovarian cancer.
 CC This sequence represents a human ovarian cancer DNA marker of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 319 BP; 77 A; 61 C; 78 G; 99 T; 0 U; 4 Other;

Query Match 1.4%; Score 24; DB 5; Length 319;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACCTCGCGCGACACGC 1713
 |||||
 Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 47
 ABQ58175
 ID ABQ58175 standard; cDNA; 320 BP.
 XX
 AC ABQ58175;
 XX

DT 02-AUG-2002 (first entry)
 XX

DE Human colon cancer related nucleotide sequence SEQ ID NO:1870.
 XX

KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;
 KW genetic analysis; diagnostic; antisense therapy; gene; ss.
 XX

OS Homo sapiens.
 XX

PN WO200229086-A2.
 XX

PD 11-APR-2002.
 XX

PF 02-OCT-2001; 2001WO-US030732.
 XX

PR 02-OCT-2000; 2000US-0237271P.
 XX

PA (FARB) BAYER CORP.
 XX

PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
 PI Thiagalingam A, Lewis ME;
 XX

DR WPI; 2002-426115/45.
 XX

PT New isolated nucleic acid that is differentially expressed in cancer

PT tissues useful for determining the presence of colon cancer in a cell or
 XX tissue type, and in antisense therapy.

PS Claim 1; Fig 1; 796pp; English.

XX ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
 CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
 CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
 CC used in antisense therapy. An antibody immunoreactive with a polypeptide
 CC encoded by (I) is useful for detecting cancer in a patient sample, and
 CC for detecting the presence or absence of a polynucleotide encoded by a
 CC nucleic acid which hybridises to (I) in a cell. A probe/primer derived
 CC from (I) can be used for determining the presence of a nucleic acid which
 CC hybridises to (I), and for determining the phenotype of cells in a sample
 CC of cells from a patient. (I) is useful for determining the presence of
 CC colon cancer in a cell or tissue type, for determining the presence or
 CC state of other type of cancer, in antisense therapy, to generate
 CC macroarrays on a solid surface, to identify a chromosome on which the
 CC corresponding gene resides, and in tissue profiling, forensics, genetic
 CC analysis, mapping and diagnostic applications. (I) can be used to raise
 CC antibodies, and to screen for peptide analogues and antagonists

XX SQ Sequence 320 BP; 66 A; 89 C; 89 G; 75 T; 0 U; 1 Other;

Query Match 1.4%; Score 24; DB 6; Length 320;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713

Db 289 TAAGTACTCGCGCGACACGC 312

RESULT 48

ADL44057/c

ID ADL44057 standard; DNA; 326 BP.

AC ADL44057;

DT 20-MAY-2004 (first entry)

DE Human ovarian cancer DNA marker #17947.

KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

OS Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-0207124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

XX 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
 XX cancer cells as compared to their normal non-cancerous ovarian cells are
 XX used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 17947; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in

CC ovarian cancer cells as compared to their expression in normal (i.e. non-
 CC cancerous) ovarian cells. The invention also relates to polypeptides
 CC encoded by the markers, antibodies that selectively bind to the
 CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
 CC of developing ovarian cancer involving inhibiting expression of a gene
 CC corresponding to a marker of the invention and a method of treating a
 CC patient afflicted with ovarian cancer comprising providing to cells of
 CC the patient an antisense oligonucleotide complementary to a marker of the
 CC invention. The markers are useful for assessing if a patient is afflicted
 CC with ovarian cancer, which involves comparing the level of expression of
 CC a marker in a patient sample and a normal level of expression of the
 CC marker in a control non-ovarian cancer sample. A difference between the
 CC expression levels indicates ovarian cancer. The level of expression of a
 CC marker corresponds to a secreted protein or to a transcribed
 CC polynucleotide or its portion. The level of expression of the marker is
 CC assessed by detecting the presence in the sample, a protein or protein
 CC fragment corresponding to the marker. The presence of protein or protein
 CC fragment is detected using an antibody that specifically binds with the
 CC protein or protein fragment. Alternatively, the level of expression of
 CC the marker is assessed by detecting the presence of a transcribed
 CC polynucleotide which anneals with the marker or anneals with a portion of
 CC the polynucleotide comprising the marker, under stringent conditions. The
 CC marker is also used for monitoring the progression of ovarian cancer in a
 CC patient which involves detecting expression of the marker in a patient
 CC sample at a first point in time, repeating the method at a subsequent
 CC time and comparing the level of expression. The method is carried out
 CC using an ovarian tissue sample. A composition comprising a marker,
 CC polypeptide or antibody of the invention is used to treat ovarian cancer.
 CC This sequence represents a human ovarian cancer DNA marker of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 326 BP; 92 A; 70 C; 47 G; 116 T; 0 U; 1 Other;

Query Match 1.4%; Score 24; DB 5; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713

Db 113 TAAGTACTCGCGCGACACGC 90

RESULT 49

AAH69655/c

ID AAH69655 standard; cDNA; 331 BP.

XX AC AAH69655;

DT 19-SEP-2001 (first entry)

XX Human cervical cancer marker nucleic acid 929.

DE Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

XX Homo sapiens.

XX WO200142467-A2.

XX 14-JUN-2001.

XX 08-DEC-2000; 2000WO-US033312.

XX 08-DEC-1999; 99US-0169681P.

XX 21-DEC-1999; 99US-0171350P.

XX 14-MAR-2000; 2000US-0189315P.

XX 12-MAY-2000; 2000US-0203791P.

XX 09-JUN-2000; 2000US-0210600P.

XX 21-JUL-2000; 2000US-0220114P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Deeds J, Berger A, Zhao X;
XX WPI; 2001-375006/39.
XX
PT New isolated nucleic acid for diagnosing and treating cervical cancer and
XX for assessing and detecting compounds for treating the cancer.
XX
PS Claim 1; Page 257-258; 1051pp; English.
XX
CC The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy
XX
SQ Sequence 331 BP; 109 A; 49 C; 59 G; 114 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTCGCGCGACCGC 1713
Db 30 TAAGTACTCTCGCGCGACCGC 7
RESULT 50
AAL13080/c
ID AAL13080 standard; cDNA; 337 BP.
AC AAL13080;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 5537.
XX
KW Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001WO-US000799.
XX
PR 14-JAN-2000; 2000US-0176077P.
PR 14-MAR-2000; 2000US-0189167P.
PR 24-MAR-2000; 2000US-0192099P.
PR 29-MAR-2000; 2000US-0193480P.
PR 15-MAY-2000; 2000US-0205230P.
PR 09-JUN-2000; 2000US-0211315P.
PR 25-JUL-2000; 2000US-0220534P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2001-451856/48.
XX
PT New peptide useful as a marker for the diagnosis of breast cancer.
XX
PS Claim 1; Page 995; 3695pp; English.
XX
CC The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and

CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity
XX
SQ Sequence 337 BP; 127 A; 63 C; 60 G; 83 T; 0 U; 4 Other;
Query Match 1.4%; Score 24; DB 4; Length 337;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTCGCGCGACCGC 1713
Db 30 TAAGTACTCTCGCGCGACCGC 7
RESULT 51
AAH69708/c
ID AAH69708 standard; cDNA; 338 BP.
AC AAH69708;
XX
DT 19-SEP-2001 (first entry)
XX
DE Human cervical cancer marker nucleic acid 982.
XX
KW Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200142467-A2.
XX
PD 14-JUN-2001.
XX
PF 08-DEC-2000; 2000WO-US033312.
XX
PR 08-DEC-1999; 99US-0169681P.
PR 21-DEC-1999; 99US-0171350P.
PR 14-MAR-2000; 2000US-0189315P.
PR 12-MAY-2000; 2000US-0203791P.
PR 09-JUN-2000; 2000US-0210600P.
PR 21-JUL-2000; 2000US-0220114P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Deeds J, Berger A, Zhao X;
XX WPI; 2001-375006/39.
XX
PT New isolated nucleic acid for diagnosing and treating cervical cancer and
XX for assessing and detecting compounds for treating the cancer.
XX
PS Claim 1; Page 264; 1051pp; English.
XX
CC The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy
XX
SQ Sequence 338 BP; 94 A; 64 C; 87 G; 93 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 4; Length 338;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTCGCGCGACCGC 1713
Db 30 TAAGTACTCTCGCGCGACCGC 7

```
RESULT 52
ID ABV08004/c
XX ABV08004 standard; cDNA; 346 BP.
AC ABV08004;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 7995.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2000160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 1280; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 346 BP; 126 A; 60 C; 57 G; 103 T; 0 U; 0 Other;
XX
Query Match 1.4%; Score 24; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1690 TAAGTACCTCGCGCGACACGC 1713
Db 30 TAAGTACCTCGCGCGACACGC 7
XX
RESULT 53
ID ADL37120/c
XX ADL37120 standard; DNA; 368 BP.
AC ADL37120;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #11010.
XX
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009126.
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 11010; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX Sequence 368 BP; 96 A; 67 C; 84 G; 120 T; 0 U; 1 Other;
XX
Query Match 1.4%; Score 24; DB 5; Length 368;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1690 TAAGTACCTCGCGCGACACGC 1713
Db 30 TAAGTACCTCGCGCGACACGC 7
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RESULT 54
ADI171969/c
ID ADI171969 standard; DNA; 368 BP.
XX AC ADI171969;
XX DT 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #4711.
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX OS Homo sapiens.
XX PN WO200170979-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009126.
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PA Lee J, Lillie J;
XX PI WPI; 2001-611502/70.
XX DR Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX PT cancer cells as compared to their normal non-cancerous ovarian cells are
XX PT used to characterize stage, grade, histological type of ovarian cancer.
XX PS Disclosure; SEQ ID NO 4711; 106pp; English.
XX CC The invention relates to nucleic acid markers which are overexpressed in
XX CC ovarian cancer cells as compared to their expression in normal (i.e. non-
XX CC cancerous) ovarian cells. The invention also relates to polypeptides
XX CC encoded by the markers, antibodies that selectively bind to the
XX CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX CC of developing ovarian cancer involving inhibiting expression of a gene
XX CC corresponding to a marker of the invention and a method of treating a
XX CC patient afflicted with ovarian cancer comprising providing to cells of
XX CC the patient an antisense oligonucleotide complementary to a marker of the
XX CC invention. The markers are useful for assessing if a patient is afflicted
XX CC with ovarian cancer, which involves comparing the level of expression of
XX CC a marker in a patient sample and a normal level of expression of the
XX CC marker in a control non-ovarian cancer sample. A difference between the
XX CC expression levels indicates ovarian cancer. The level of expression of a
XX CC marker corresponds to a secreted protein or to a transcribed
XX CC polynucleotide or its portion. The level of expression of the marker is
XX CC assessed by detecting the presence in the sample, a protein or protein
XX CC fragment corresponding to the marker. The presence of protein or protein
XX CC fragment is detected using an antibody that specifically binds with the
XX CC protein or protein fragment. Alternatively, the level of expression of
XX CC the marker is assessed by detecting the presence of a transcribed
XX CC polynucleotide which anneals with the marker or anneals with a portion of
XX CC the polynucleotide comprising a marker, under stringent conditions. The
XX CC marker is also used for monitoring the progression of ovarian cancer in a
XX CC patient which involves detecting expression of the marker in a patient
XX CC sample at a first point in time, repeating the method at a subsequent
XX CC time and comparing the level of expression. The method is carried out
XX CC using an ovarian tissue sample. A composition comprising a marker,
XX CC polypeptide or antibody of the invention is used to treat ovarian cancer.
XX CC This sequence represents a human ovarian cancer DNA marker of the
XX CC invention. Note: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQL Sequence 368 BP; 96 A; 67 C; 84 G; 120 T; 0 U; 1 Other;
Query Match 1.4%; Score 24; DB 5; Length 368;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAACTACTCTGGCGCGGACCGC 1713
DB 30 TAACTACTCTGGCGCGGACCGC 7
RESULT 55
ADI73216/c
ID ADI73216 standard; DNA; 370 BP.
XX AC ADI73216;
XX DT 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #5958.
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX OS Homo sapiens.
XX PN WO200170979-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009126.
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PA Lee J, Lillie J;
XX PI WPI; 2001-611502/70.
XX DR Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX PT cancer cells as compared to their normal non-cancerous ovarian cells are
XX PT used to characterize stage, grade, histological type of ovarian cancer.
XX PS Disclosure; SEQ ID NO 5958; 106pp; English.
XX CC The invention relates to nucleic acid markers which are overexpressed in
XX CC ovarian cancer cells as compared to their expression in normal (i.e. non-
XX CC cancerous) ovarian cells. The invention also relates to polypeptides
XX CC encoded by the markers, antibodies that selectively bind to the
XX CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX CC of developing ovarian cancer involving inhibiting expression of a gene
XX CC corresponding to a marker of the invention and a method of treating a
XX CC patient afflicted with ovarian cancer comprising providing to cells of
XX CC the patient an antisense oligonucleotide complementary to a marker of the
XX CC invention. The markers are useful for assessing if a patient is afflicted
XX CC with ovarian cancer, which involves comparing the level of expression of
XX CC a marker in a patient sample and a normal level of expression of the
XX CC marker in a control non-ovarian cancer sample. A difference between the
XX CC expression levels indicates ovarian cancer. The level of expression of a
XX CC marker corresponds to a secreted protein or to a transcribed
XX CC polynucleotide or its portion. The level of expression of the marker is
XX CC assessed by detecting the presence in the sample, a protein or protein
XX CC fragment corresponding to the marker. The presence of protein or protein
XX CC fragment is detected using an antibody that specifically binds with the
XX CC protein or protein fragment. Alternatively, the level of expression of
XX CC the marker is assessed by detecting the presence of a transcribed
XX CC polynucleotide which anneals with the marker or anneals with a portion of
XX CC the polynucleotide comprising the marker, under stringent conditions. The

CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX Sequence 370 BP; 131 A; 76 C; 61 G; 96 T; 0 U; 6 Other;

Query Match 1.4%; Score 24; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGCG 1713
|||||
Db 30 TAAGTACTCGCGCGACACGCG 7

RESULT 56
ADL38348/c
ID ADL38348 standard; DNA; 370 BP.
XX AC ADL38348;
XX AC
XX DT 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #12238.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009126.
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-02071124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 12238; 106pp; English.
XX

XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a

CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX Sequence 370 BP; 131 A; 76 C; 61 G; 96 T; 0 U; 6 Other;

Query Match 1.4%; Score 24; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGCG 1713
|||||
Db 30 TAAGTACTCGCGCGACACGCG 7

RESULT 57
ABV06075/c
ID ABV06075 standard; cDNA; 376 BP.
XX AC ABV06075;
XX 13-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 6066.
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX Homo sapiens.
XX WO200160860-A2.
XX 23-AUG-2001.
XX 20-FEB-2001; 2001WO-US005171.
XX 17-FEB-2000; 2000US-0183319P.
XX 16-MAR-2000; 2000US-0189852P.
XX 25-MAY-2000; 2000US-0207454P.
XX 09-JUN-2000; 2000US-0211314P.
XX 18-JUL-2000; 2000US-0219007P.
XX 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX Claim 1; Page 1006; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the

CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX

Sequence 376 BP; 122 A; 55 C; 63 G; 136 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 376;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713

Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 58

ADL42875/c

ID ADL42875 standard; DNA; 382 BP.

XX AC ADL42875;

XX DT 20-MAY-2004 (first entry)

XX DE Human ovarian cancer DNA marker #16765.

XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX OS Homo sapiens.

XX PN WO200170979-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US009126.

XX PR 21-MAR-2000; 2000US-0191031P.

XX PR 25-MAY-2000; 2000US-0207124P.

XX PR 15-JUN-2000; 2000US-0211940P.

XX PR 07-JUL-2000; 2000US-02116820P.

XX PR 25-JUL-2000; 2000US-0220661P.

XX PR 21-DEC-2000; 2000US-0257672P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Lee J, Lillie J;

XX DR WPI; 2001-611502/70.

XX PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
 PT cancer cells as compared to their normal non-cancerous ovarian cells are
 PT used to characterize stage, grade, histological type of ovarian cancer.

XX PS Disclosure; SEQ ID NO 16765; 106pp; English.

XX CC The invention relates to nucleic acid markers which are overexpressed in
 CC ovarian cancer cells as compared to their expression in normal (i.e. non-
 CC cancerous) ovarian cells. The invention also relates to polypeptides
 CC encoded by the markers, antibodies that selectively bind to the
 CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
 CC of developing ovarian cancer involving inhibiting expression of a gene
 CC corresponding to a marker of the invention and a method of treating a
 CC patient afflicted with ovarian cancer comprising providing to cells of
 CC the patient an antisense oligonucleotide complementary to a marker of the
 CC invention. The markers are useful for assessing if a patient is afflicted
 CC with ovarian cancer, which involves comparing the level of expression of
 CC a marker in a patient sample and a normal level of expression of the
 CC marker in a control non-ovarian cancer sample. A difference between the
 CC expression levels indicates ovarian cancer. The level of expression of a

CC marker corresponds to a secreted protein or to a transcribed
 CC polynucleotide or its portion. The level of expression of the marker is
 CC assessed by detecting the presence in the sample, a protein or protein
 CC fragment corresponding to the marker. The presence of protein or protein
 CC fragment is detected using an antibody that specifically binds with the
 CC protein or protein fragment. Alternatively, the level of expression of
 CC the marker is assessed by detecting the presence of a transcribed
 CC polynucleotide which anneals with the marker or anneals with a portion of
 CC the polynucleotide comprising the marker, under stringent conditions. The
 CC marker is also used for monitoring the progression of ovarian cancer in a
 CC patient which involves detecting expression of the marker in a patient
 CC sample at a first point in time, repeating the method at a subsequent
 CC time and comparing the level of expression. The method is carried out
 CC using an ovarian tissue sample. A composition comprising a marker,
 CC polypeptide or antibody of the invention is used to treat ovarian cancer.
 CC This sequence represents a human ovarian cancer DNA marker of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 382 BP; 113 A; 69 C; 70 G; 130 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 382;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713

Db 101 TAAGTACCTCGCGCGACACGC 78

RESULT 59

ADI76489/c

ID ADI76489 standard; DNA; 391 BP.

XX AC ADI76489;

XX DT 20-MAY-2004 (first entry)

XX DE Human ovarian cancer DNA marker #9231.

XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX OS Homo sapiens.

XX PN WO200170979-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US009126.

XX PR 21-MAR-2000; 2000US-0191031P.

XX PR 25-MAY-2000; 2000US-0207124P.

XX PR 15-JUN-2000; 2000US-0211940P.

XX PR 07-JUL-2000; 2000US-02116820P.

XX PR 25-JUL-2000; 2000US-0220661P.

XX PR 21-DEC-2000; 2000US-0257672P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Lee J, Lillie J;

XX DR WPI; 2001-611502/70.

XX PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
 PT cancer cells as compared to their normal non-cancerous ovarian cells are
 PT used to characterize stage, grade, histological type of ovarian cancer.

XX PS Disclosure; SEQ ID NO 9231; 106pp; English.

XX CC The invention relates to nucleic acid markers which are overexpressed in
 CC ovarian cancer cells as compared to their expression in normal (i.e. non-
 CC cancerous) ovarian cells. The invention also relates to polypeptides

CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 391 BP; 180 A; 42 C; 53 G; 116 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 60
AD170160/c
ID AD170160 standard; DNA; 391 BP.
XX
AC AD170160;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #2902.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
PN WO200170979-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
FR 25-MAY-2000; 2000US-0207124P.
FR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
FA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
FI Lee J, Lillie J;
XX

DR WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
PS Disclosure; SEQ ID NO 2902; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX Sequence 391 BP; 180 A; 42 C; 53 G; 116 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 61
ADL42485/c
ID ADL42485 standard; DNA; 391 BP.
XX
AC ADL42485;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #16375.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
PN WO200170979-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.

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PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 16375; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 391 BP; 90 A; 74 C; 90 G; 137 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 391;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1690 TAAGTACTCTCGCGCGACACGC 1713
XX Db |||||||||||||||||||
XX 110 TAAGTACTCTCGCGCGACACGC 87
XX
XX RESULT 62
XX ADI76850/c
XX ID ADI76850 standard; DNA; 392 BP.
XX
XX ADI76850;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human ovarian cancer DNA marker #9592.
XX
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
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XX OS Homo sapiens.
XX PN WO200170979-A2.
XX PD 27-SEP-2001.
XX
XX PF 21-MAR-2001; 2001WO-US009126.
XX
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 9592; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 392 BP; 115 A; 50 C; 78 G; 146 T; 0 U; 3 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 392;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1690 TAAGTACTCTCGCGCGACACGC 1713
XX Db |||||||||||||||||||
XX 30 TAAGTACTCTCGCGCGACACGC 7
XX
XX RESULT 63
XX ADI70525/c
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ID ADI70525 standard; DNA; 392 BP.
XX
AC ADI70525;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #3267.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
FN WO200170979-A2.
XX
PD 27-SEP-2001.
XX
FF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lee J, Lillie J;
XX
WPI; 2001-611502/70.
DR
XX
PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
FS Disclosure; SEQ ID NO 3267; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 392 BP; 115 A; 50 C; 78 G; 146 T; 0 U; 3 Other;

Query Match 1.4%; Score 24; DB 5; Length 392;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGCACCACGC 1713
Db 30 TAAGTACTCGCGCGCACCACGC 7
RESULT 64
ABV08052/c
ID ABV08052 standard; cDNA; 404 BP.
XX
AC ABV08052;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 8043.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
FN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
FF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 1286; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 404 BP; 130 A; 76 C; 42 G; 153 T; 0 U; 3 Other;
Query Match 1.4%; Score 24; DB 5; Length 404;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGCACCACGC 1713
Db 30 TAAGTACTCGCGCGCACCACGC 7

RESULT 65
ADL42159/c
ID ADL42159 standard; DNA; 409 BP.
XX AC ADL42159;
XX DT 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #16049.
XX DE Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX OS Homo sapiens.
XX PN WO200170979-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009126.
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 16049; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 409 BP; 124 A; 85 C; 90 G; 110 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 5; Length 409;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTCGCGCGGACACGC 1713
DB 111 TAAGTACTCTCGCGCGGACACGC 88
RESULT 66
ADL43269/c
ID ADL43269 standard; DNA; 415 BP.
XX AC ADL43269;
XX DT 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #17159.
XX DE Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX OS Homo sapiens.
XX PN WO200170979-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009126.
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 17159; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The

CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 415 BP; 140 A; 73 C; 92 G; 110 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 415;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCGCGCGACACG 1713

|||||

Db 111 TAAGTACTCGCGCGACACG 88

RESULT 67

ADL37618/c

ID ADL37618 standard; DNA; 416 BP.

XX AC ADL37618;

XX DT 20-MAY-2004 (first entry)

XX DE Human ovarian cancer DNA marker #11508.

XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX OS Homo sapiens.

XX PN WO200170979-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US009126.

XX PR 21-MAR-2000; 2000US-0191031P.

XX PR 25-MAY-2000; 2000US-0207124P.

XX PR 15-JUN-2000; 2000US-0211940P.

XX PR 07-JUL-2000; 2000US-0216820P.

XX PR 25-JUL-2000; 2000US-0220661P.

XX PR 21-DEC-2000; 2000US-0257672P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Lee J, Lillie J;

XX DR WPI; 2001-611502/70.

XX PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.

XX PS Disclosure; SEQ ID NO 11508; 106pp; English.

XX
CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the

CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX SQ Sequence 416 BP; 128 A; 97 C; 62 G; 128 T; 0 U; 1 Other;

Query Match 1.4%; Score 24; DB 5; Length 416;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCGCGCGACACG 1713

|||||

Db 30 TAAGTACTCGCGCGACACG 7

RESULT 68

ADI72479/c

ID ADI72479 standard; DNA; 416 BP.

XX AC ADI72479;

XX DT 20-MAY-2004 (first entry)

XX DE Human ovarian cancer DNA marker #5221.

XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX OS Homo sapiens.

XX PN WO200170979-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US009126.

XX PR 21-MAR-2000; 2000US-0191031P.

XX PR 25-MAY-2000; 2000US-0207124P.

XX PR 15-JUN-2000; 2000US-0211940P.

XX PR 07-JUL-2000; 2000US-0216820P.

XX PR 25-JUL-2000; 2000US-0220661P.

XX PR 21-DEC-2000; 2000US-0257672P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Lee J, Lillie J;

XX DR WPI; 2001-611502/70.

XX PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.

XX PS Disclosure; SEQ ID NO 5221; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides

CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 416 BP; 128 A; 97 C; 62 G; 128 T; 0 U; 1 Other;

Query Match 1.4%; Score 24; DB 5; Length 416;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTGGCGCGACCAAGC 1713
Db 30 TAAGTACTCTGGCGCGACCAAGC 7

RESULT 69

ADL38889
ID ADL38889 standard; DNA; 420 BP.

AC ADL38889;

DT 20-MAY-2004 (first entry)

DE Human ovarian cancer DNA marker #12779.

Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

OS Homo sapiens.

PN WO200170979-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US009126.

PR 21-MAR-2000; 2000US-0191031P.

PR 25-MAY-2000; 2000US-0207124P.

PR 15-JUN-2000; 2000US-0211940P.

PR 07-JUL-2000; 2000US-0216820P.

PR 25-JUL-2000; 2000US-0220661P.

PR 21-DEC-2000; 2000US-0257672P.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Lee J, Lillie J;

XX

DR WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.

PS Disclosure; SEQ ID NO 12779; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 420 BP; 126 A; 77 C; 77 G; 140 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTGGCGCGACCAAGC 1713

Db 391 TAAGTACTCTGGCGCGACCAAGC 414

RESULT 70

ADL41799/c

ID ADL41799 standard; DNA; 420 BP.

AC ADL41799;

DT 20-MAY-2004 (first entry)

DE Human ovarian cancer DNA marker #15689.

Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

OS Homo sapiens.

PN WO200170979-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US009126.

XX


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PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX
XX Lee J, Lillie J;
XX
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 15689; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX expression levels indicates ovarian cancer. A difference between the
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 420 BP; 102 A; 83 C; 111 G; 124 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 420;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1690 TAAGTACCTCGCGCGGACACGC 1713
XX |
XX 111 TAAGTACCTCGCGCGGACACGC 88
XX
XX RESULT 71
XX ADI73071
XX ID ADI73071 standard; DNA; 421 BP.
XX
XX AC ADI73071;
XX
XX XX 20-MAY-2004 (first entry)
XX
XX DE Human ovarian cancer DNA marker #5813.
XX
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
XX Homo sapiens.
XX
XX WO200170979-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 5813; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX expression levels indicates ovarian cancer. A difference between the
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 421 BP; 126 A; 77 C; 78 G; 140 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 421;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1690 TAAGTACCTCGCGCGGACACGC 1713
XX |
XX 391 TAAGTACCTCGCGCGGACACGC 414
XX
XX Db
```

RESULT 72
ABV39230/c
ID ABV39230 standard; cDNA; 424 BP.
XX
AC ABV39230;
XX
DT 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 39221.
XX
DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
OS
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX
XX 17-FEB-2000; 2000US-0183319P.
PR
XX 16-MAR-2000; 2000US-0189862P.
PR
XX 25-MAY-2000; 2000US-0207454P.
PR
XX 09-JUN-2000; 2000US-0211314P.
PR
XX 18-JUL-2000; 2000US-0219007P.
PR
XX 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
PI
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 7963; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 424 BP; 120 A; 97 C; 88 G; 119 T; 0 U; 0 Other;
XX
Query Match 1.4%; Score 24; DB 5; Length 424;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 85 TAAGTACCTCGCGCGGACACGC 62
XX
RESULT 73
ACN86430/c
ID ACN86430 standard; DNA; 425 BP.
XX
AC ACN86430;
XX
DT 02-DEC-2004 (first entry)

XX Breast cancer related marker, seq id 7580.
DE
XX Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
KW
XX Homo sapiens.
OS
XX US2003099974-A1.
PN
XX 29-MAY-2003.
PD
XX 18-JUL-2002; 2002US-00198846.
PF
XX 18-JUL-2001; 2001US-0306220P.
PR
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Lillie J, Xu Y, Wang Y, Steinmann K;
PI
XX WPI; 2003-787014/74.
XX
XX Novel isolated polypeptide associated with breast cancer, useful for
PT detecting presence of polypeptide in sample, as a marker for breast
PT cancer.
XX
XX Disclosure; SEQ ID NO 7580; 36pp; English.
XX
CC The invention relates to an isolated polypeptide (I) associated with
CC breast cancer which is encoded by a nucleic acid molecule comprising a
CC nucleotide sequence (SI). Further disclosed is an antibody that binds to
CC the polypeptide of the invention. The activity of the polypeptide of the
CC invention may be described as cytostatic. The antibody is useful for
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC invention are useful in the detection of breast tumours. (I) is useful as
CC a marker for breast cancer and in breast cancer therapy. Sequences given
CC in records ACN78851-ACN92934 represent nucleic acid markers associated
CC with breast cancer. Note: The sequence listing does not form part of the
CC specification but may be obtained in electronic format from the USPTO web
CC site at seqdata.uspto.gov/sequence.html?docID=20030099974
XX
SQ Sequence 425 BP; 136 A; 92 C; 90 G; 106 T; 0 U; 1 Other;
XX
Query Match 1.4%; Score 24; DB 11; Length 425;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 105 TAAGTACCTCGCGCGGACACGC 82
XX
RESULT 74
ABV06575/c
ID ABV06575 standard; cDNA; 426 BP.
XX
XX AC ABV06575;
XX
XX 13-SEP-2002 (first entry)
DT
XX Human prostate expression marker cDNA 6566.
DE
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
OS
XX WO200160860-A2.
PN
XX 23-AUG-2001.
PD
XX 20-FEB-2001; 2001WO-US005171.
PF
XX 17-FEB-2000; 2000US-0183319P.
PR

```
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 1075; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 426 BP; 116 A; 102 C; 110 G; 98 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 426;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1690 TAAGTACCTCGCGCGACACGC 1713
XX |||||
XX Db 30 TAAGTACCTCGCGCGACACGC 7
XX
XX RESULT 75
XX ADL44606/C
XX ID ADL44606 standard; DNA; 426 BP.
XX
XX AC ADL44606;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human ovarian cancer DNA marker #18496.
XX
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
XX OS Homo sapiens.
XX
XX PN WO200170979-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 21-MAR-2001; 2001WO-US009126.
XX
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX
XX
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DR WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 18496; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX
XX Sequence 426 BP; 176 A; 51 C; 47 G; 152 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 426;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1690 TAAGTACCTCGCGCGACACGC 1713
XX |||||
XX Db 111 TAAGTACCTCGCGCGACACGC 88
XX
XX RESULT 76
XX ABV37925/C
XX ID ABV37925 standard; cDNA; 432 BP.
XX
XX AC ABV37925;
XX
XX DT 16-SEP-2002 (first entry)
XX
XX DE Human prostate expression marker cDNA 37916.
XX
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200160860-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 20-FEB-2001; 2001WO-US005171.
XX
XX PR 17-FEB-2000; 2000US-0183319P.
XX
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PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 7755; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 432 BP; 153 A; 67 C; 75 G; 137 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 432;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 56 TAAGTACCTCGCGCGGACACGC 33
XX
RESULT 77
ADL44732/c
ID ADL44732 standard; DNA; 432 BP.
XX
XX ADL44732;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human ovarian cancer DNA marker #18622.
XX
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
XX Homo sapiens.
XX
XX WO200170979-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX
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DR WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 18622; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX
XX Sequence 432 BP; 146 A; 93 C; 81 G; 112 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 432;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 95 TAAGTACCTCGCGCGGACACGC 72
XX
RESULT 78
ADI70358/c
ID ADI70358 standard; DNA; 437 BP.
XX
XX AC ADI70358;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human ovarian cancer DNA marker #3100.
XX
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
XX Homo sapiens.
XX
XX WO200170979-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
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PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
PI Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 3100; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX
XX Sequence 437 BP; 102 A; 88 C; 91 G; 150 T; 0 U; 6 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 437;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1690 TAAGTACTCTCGCGCGACCAACGC 1713
XX |||||||
XX Db 30 TAAGTACTCTCGCGCGACCAACGC 7
XX
XX RESULT 79
XX ADI76684/c
XX ID ADI76684 standard; DNA; 437 BP.
XX
XX AC ADI76684;
XX
XX XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human ovarian cancer DNA marker #9426.
XX
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
XX OS Homo sapiens.
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XX WO200170979-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 21-MAR-2001; 2001WO-US009126.
XX
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX PI Lee J, Lillie J;
XX
XX DR WPI; 2001-611502/70.
XX
XX PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX PS Disclosure; SEQ ID NO 9426; 106pp; English.
XX
XX CC The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX
XX Sequence 437 BP; 102 A; 88 C; 91 G; 150 T; 0 U; 6 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 437;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1690 TAAGTACTCTCGCGCGACCAACGC 1713
XX |||||||
XX Db 30 TAAGTACTCTCGCGCGACCAACGC 7
XX
XX RESULT 80
XX ADL44126/c
XX ID ADL44126 standard; DNA; 442 BP.
XX
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AC ADL44126;
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #18016.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009126.
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 18016; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX Sequence 442 BP; 116 A; 104 C; 111 G; 111 T; 0 U; 0 Other;
XX Query Match 1.4%; Score 24; DB 5; Length 442;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 444 BP; 152 A; 77 C; 116 G; 99 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 444;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 73 TAAGTACCTCGCGCGGACACGC 50

RESULT 82
ABV36041/c
ID ABV36041 standard; cDNA; 446 BP.

XX AC ABV36041;

XX DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 36032.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX DR WPI; 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 7471; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 446 BP; 137 A; 71 C; 85 G; 153 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 101 TAAGTACCTCGCGCGGACACGC 78

RESULT 83
ABV37972/c
ID ABV37972 standard; cDNA; 446 BP.
XX AC ABV37972;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 37963.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX DR WPI; 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 7762; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 446 BP; 139 A; 86 C; 56 G; 165 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 71 TAAGTACCTCGCGCGGACACGC 48

RESULT 84
ABV45101/c


```
ID  ABV45101 standard; cDNA; 446 BP.
XX
AC  ABV45101;
XX
XX  16-SEP-2002 (first entry)
XX
XX  Human prostate expression marker cDNA 45092.
XX
XX  Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW  pharmacogenomic marker; gene; ss.
XX
XX  Homo sapiens.
XX
XX  WO200150860-A2.
XX
XX  23-AUG-2001.
XX
XX  20-FEB-2001; 2001WO-US005171.
XX
XX  17-FEB-2000; 2000US-0183319P.
XX
XX  16-MAR-2000; 2000US-0189862P.
XX
XX  25-MAY-2000; 2000US-0207454P.
XX
XX  09-JUN-2000; 2000US-0211314P.
XX
XX  18-JUL-2000; 2000US-0219007P.
XX
XX  13-DEC-2000; 2000US-0253281P.
XX
XX  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX  Schlegel R, Endege WO, Monahan JB;
XX
XX  WPI; 2001-662795/76.
XX
XX  Novel isolated nucleic acid molecule associated with cancerous state of
PT  prostate cells and correlating with presence of prostate cancer, useful
PT  for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX  Claim 1; Page 8933; 11750pp; English.
XX
XX  The invention relates to an isolated nucleic acid molecule (I) comprising
CC  a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC  specification or its complement. (I) is useful for: (a) assessing whether
CC  a patient is afflicted with prostate cancer; (b) monitoring the
CC  progression of prostate cancer in a patient; (c) assessing the efficacy
CC  of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC  the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC  (e) selecting a composition for inhibiting prostate cancer in a patient;
CC  (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC  determining whether prostate cancer has metastasized in a patient; (h)
CC  assessing the aggressiveness or indolence of prostate cancer in a patient
CC  ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX  Sequence 446 BP; 137 A; 71 C; 85 G; 153 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 24; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 101 TAAGTACCTCGCGCGGACACGC 78
RESULT 85
ADL36720/c
ID ADL36720 standard; DNA; 446 BP.
XX
XX ADL36720;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human ovarian cancer DNA marker #10610.
XX
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
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XX Homo sapiens.
OS WO200170979-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
XX
XX 25-MAY-2000; 2000US-0207124P.
XX
XX 15-JUN-2000; 2000US-0211940P.
XX
XX 07-JUL-2000; 2000US-0216820P.
XX
XX 25-JUL-2000; 2000US-0220661P.
XX
XX 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT  cancer cells as compared to their normal non-cancerous ovarian cells are
PT  used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 10610; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
CC  ovarian cancer cells as compared to their expression in normal (i.e. non-
CC  cancerous) ovarian cells. The invention also relates to polypeptides
CC  encoded by the markers, antibodies that selectively bind to the
CC  polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC  of developing ovarian cancer involving inhibiting expression of a gene
CC  corresponding to a marker of the invention and a method of treating a
CC  patient afflicted with ovarian cancer comprising providing to cells of
CC  the patient an antisense oligonucleotide complementary to a marker of the
CC  invention. The markers are useful for assessing if a patient is afflicted
CC  with ovarian cancer, which involves comparing the level of expression of
CC  a marker in a patient sample and a normal level of expression of the
CC  marker in a control non-ovarian cancer sample. A difference between the
CC  expression levels indicates ovarian cancer. The level of expression of a
CC  marker corresponds to a secreted protein or to a transcribed
CC  polynucleotide or its portion. The level of expression of the marker is
CC  assessed by detecting the presence in the sample, a protein or protein
CC  fragment corresponding to the marker. The presence of protein or protein
CC  fragment is detected using an antibody that specifically binds with the
CC  protein or protein fragment. Alternatively, the level of expression of
CC  the marker is assessed by detecting the presence of a transcribed
CC  polynucleotide which anneals with the marker or anneals with a portion of
CC  the polynucleotide comprising the marker, under stringent conditions. The
CC  marker is also used for monitoring the progression of ovarian cancer in a
CC  patient which involves detecting expression of the marker in a patient
CC  sample at a first point in time, repeating the method at a subsequent
CC  time and comparing the level of expression. The method is carried out
CC  using an ovarian tissue sample. A composition comprising a marker,
CC  polypeptide or antibody of the invention is used to treat ovarian cancer.
CC  This sequence represents a human ovarian cancer DNA marker of the
CC  invention.
XX
XX Sequence 446 BP; 123 A; 114 C; 85 G; 123 T; 0 U; 1 Other;
SQ
Query Match 1.4%; Score 24; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 30 TAAGTACCTCGCGCGGACACGC 7
RESULT 86
ADI71564/c
```

ID ADI71564 standard; DNA; 446 BP.
XX AC ADI71564;
XX DT 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #4306.
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX OS Homo sapiens.
XX PN WO200170979-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009126.
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lee J, Lillie J;
XX WPI; 2001-611502/70.

Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

Disclosure; SEQ ID NO 4306; 106bp; English.

The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention.

XX SQ Sequence 446 BP; 123 A; 114 C; 85 G; 123 T; 0 U; 1 Other;
Query Match 1.4%; Score 24; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAGTACCTCGCGCGGACCAAGC 1713
Db 30 TAGTACCTCGCGCGGACCAAGC 7
RESULT 87
ID ABA11128/c
XX ID ABA11128 standard; cDNA; 449 BP.
XX AC ABA11128;
XX DT 23-JAN-2002 (first entry)
XX DE Human nervous system related polynucleotide SEQ ID NO 135.
XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antiepileptic; antianemic; antirheumatic; cancer;
XX KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
XX KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
XX OS Homo sapiens.
XX PN WO200159063-A2.
XX PD 16-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US001334.
XX PR 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 24-FEB-2000; 2000US-0184664P.
XX PR 02-MAR-2000; 2000US-0186350P.
XX PR 16-MAR-2000; 2000US-0189874P.
XX PR 17-MAR-2000; 2000US-0190076P.
XX PR 18-APR-2000; 2000US-0198123P.
XX PR 19-MAY-2000; 2000US-0205515P.
XX PR 07-JUN-2000; 2000US-0209467P.
XX PR 28-JUN-2000; 2000US-0214886P.
XX PR 30-JUN-2000; 2000US-0215135P.
XX PR 07-JUL-2000; 2000US-0216647P.
XX PR 07-JUL-2000; 2000US-0216880P.
XX PR 11-JUL-2000; 2000US-0217487P.
XX PR 11-JUL-2000; 2000US-0217496P.
XX PR 14-JUL-2000; 2000US-0218290P.
XX PR 26-JUL-2000; 2000US-0220963P.
XX PR 26-JUL-2000; 2000US-0220964P.
XX PR 14-AUG-2000; 2000US-0224518P.
XX PR 14-AUG-2000; 2000US-0224519P.
XX PR 14-AUG-2000; 2000US-0225213P.
XX PR 14-AUG-2000; 2000US-0225214P.
XX PR 14-AUG-2000; 2000US-0225266P.
XX PR 14-AUG-2000; 2000US-0225267P.
XX PR 14-AUG-2000; 2000US-0225268P.
XX PR 14-AUG-2000; 2000US-0225270P.
XX PR 14-AUG-2000; 2000US-0225447P.
XX PR 14-AUG-2000; 2000US-0225757P.
XX PR 14-AUG-2000; 2000US-0225758P.
XX PR 14-AUG-2000; 2000US-0225759P.
XX PR 18-AUG-2000; 2000US-0226279P.
XX PR 22-AUG-2000; 2000US-0226681P.
XX PR 22-AUG-2000; 2000US-0226686P.
XX PR 23-AUG-2000; 2000US-0227182P.
XX PR 23-AUG-2000; 2000US-0227009P.
XX PR 30-AUG-2000; 2000US-0228924P.
XX PR 01-SEP-2000; 2000US-0229287P.
XX PR 01-SEP-2000; 2000US-0229343P.
XX PR 01-SEP-2000; 2000US-0229344P.
XX PR 01-SEP-2000; 2000US-0229345P.


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XX DE Human lung specific nucleic acid sequence SEQ ID NO:66.
XX KW Human; lung; lung specific nucleic acid; LSNAs; lung specific protein;
XX LW LSP; cytostatic; gene therapy; vaccine; metastasis; lung cancer;
XX KW squamous cell carcinoma; gene; chromosome 8; ss.
XX OS Homo sapiens.
XX XX WO200264788-A2.
XX PN 22-AUG-2002.
XX PD 20-NOV-2001; 2001WO-US045080.
XX PF 20-NOV-2000; 2000US-0252054P.
XX PR (DIAD-) DIADEXUS INC.
XX PA Macina RA, Recipon H, Chen S, Sun Y, Liu C;
XX PI WPI; 2002-657601/70.
XX DR
XX PT New lung specific nucleic acid useful in gene therapy or as vaccines for
XX PT treating lung cancer (e.g. squamous cell carcinoma) or non-carcinoma lung
XX PT diseases, as well as for diagnosing, monitoring or staging these
XX PT diseases.
XX PS Claim 1; Page 186; 282pp; English.
XX XX
XX CC The present invention describes an isolated lung specific nucleic acid
XX CC (LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid
XX CC sequences comprising 17 - 733 amino acids, given in ABP52873 to ABP52965;
XX CC (b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp),
XX CC given in ABQ75262 to ABQ75376; (c) selectively hybridizes to (a) or (b);
XX CC or (d) has 60 % sequence identity to (a) or (b). LSNA and lung specific
XX CC protein (LSP) sequences have cytostatic activity and can be used in gene
XX CC therapy and vaccines. LSNAs and LSPs are useful for diagnosing and
XX CC monitoring the presence and metastases of lung cancer in a patient. An
XX CC antibody that specifically binds to an LSP can be used for determining
XX CC the presence of an LSP in a sample, as well as for treating a patient
XX CC with lung cancer, particularly by inducing an immune response against the
XX CC lung cancer cell expressing the LSNAs or LSPs. In particular, these LSNAs
XX CC and LSPs are useful for identifying, diagnosing, monitoring, staging,
XX CC imaging and treating lung cancer (e.g. squamous cell carcinoma) and non-
XX CC cancerous disease states in lung
XX CC
XX SQ Sequence 457 BP; 163 A; 70 C; 100 G; 124 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 6; Length 457;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTCGCGCGACACGC 1713
Db 24 TAAGTACTCTCGCGCGACACGC 1
|||||
RESULT 89
ADL44815/c
ID ADL44815 standard; DNA; 460 BP.
XX AC ADL44815;
XX XX 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #18705.
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX OS Homo sapiens.
XX XX WO200170979-A2.
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XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009126.
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lee J, Lillie J;
XX DR WPI; 2001-611502/70.
XX XX
XX PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX PT cancer cells as compared to their normal non-carcinoma ovarian cells are
XX PT used to characterize stage, grade, histological type of ovarian cancer.
XX PS Disclosure; SEQ ID NO 18705; 106pp; English.
XX XX
XX CC The invention relates to nucleic acid markers which are overexpressed in
XX CC ovarian cancer cells as compared to their expression in normal (i.e. non-
XX CC cancerous) ovarian cells. The invention also relates to polypeptides
XX CC encoded by the markers, antibodies that selectively bind to the
XX CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX CC of developing ovarian cancer involving inhibiting expression of a gene
XX CC corresponding to a marker of the invention and a method of treating a
XX CC patient afflicted with ovarian cancer comprising providing to cells of the
XX CC invention the markers are useful for assessing if a patient is afflicted
XX CC with ovarian cancer, which involves comparing the level of expression of
XX CC a marker in a patient sample and a normal level of expression of the
XX CC marker in a control non-ovarian cancer sample. A difference between the
XX CC expression levels indicates ovarian cancer. The level of expression of a
XX CC marker corresponds to a secreted protein or to a transcribed
XX CC polynucleotide or its portion. The level of expression of the marker is
XX CC assessed by detecting the presence in the sample, a protein or protein
XX CC fragment corresponding to the marker. The presence of protein or protein
XX CC fragment is detected using an antibody that specifically binds with the
XX CC protein or protein fragment. Alternatively, the level of expression of
XX CC the marker is assessed by detecting the presence of a transcribed
XX CC polynucleotide which anneals with the marker or anneals with a portion of
XX CC the polynucleotide comprising the marker, under stringent conditions. The
XX CC marker is also used for monitoring the progression of ovarian cancer in a
XX CC patient which involves detecting expression of the marker in a patient
XX CC sample at a first point in time, repeating the method at a subsequent
XX CC time and comparing the level of expression. The method is carried out
XX CC using an ovarian tissue sample. A composition comprising a marker,
XX CC polypeptide or antibody of the invention is used to treat ovarian cancer.
XX CC This sequence represents a human ovarian cancer DNA marker of the
XX CC invention. Note: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 460 BP; 92 A; 98 C; 103 G; 167 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 5; Length 460;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTCGCGCGACACGC 1713
Db 108 TAAGTACTCTCGCGCGACACGC 85
|||||
RESULT 90
ACN84351/c
ID ACN84351 standard; DNA; 463 BP.
XX XX
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AC ACN84351;
XX 02-DEC-2004 (first entry)
XX Breast cancer related marker, seq id 5501.
XX Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
XX Homo sapiens.
OS US2003099974-A1.
XX 29-MAY-2003.
XX 18-JUL-2002; 2002US-00198846.
XX 18-JUL-2001; 2001US-0306220P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2003-787014/74.
XX Novel isolated polypeptide associated with breast cancer, useful for
XX detecting presence of polypeptide in sample, as a marker for breast
XX cancer.
XX Disclosure; SEQ ID NO 5501; 36pp; English.
XX The invention relates to an isolated polypeptide (I) associated with
XX breast cancer which is encoded by a nucleic acid molecule comprising a
XX nucleotide sequence (S1). Further disclosed is an antibody that binds to
XX the polypeptide of the invention. The activity of the polypeptide of the
XX invention may be described as cytostatic. The antibody is useful for
XX detecting the presence of (I) in a sample. Nucleic acid molecules of the
XX invention are useful in the detection of breast tumours. (I) is useful as
XX a marker for breast cancer and in breast cancer therapy. Sequences given
XX in records ACN78851-ACN92934 represent nucleic acid markers associated
XX with breast cancer. Note: The sequence listing does not form part of the
XX specification but may be obtained in electronic format from the USPTO web
XX site at seqdata.uspto.gov/sequence.html?DocID=20030099974
XX
SQ Sequence 463 BP; 105 A; 124 C; 116 G; 109 T; 0 U; 9 Other;
Query Match 1.4%; Score 24; DB 11; Length 463;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACCTCGCGCGGACCGC 1713
DB 116 TAAGTACCTCGCGCGGACCGC 93
RESULT 91
ADI70602/c
ID ADI70602 standard; DNA; 464 BP.
XX
AC ADI70602;
XX
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #3344.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 3344; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker, cancer
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX
SQ Sequence 464 BP; 146 A; 91 C; 92 G; 116 T; 0 U; 19 Other;
Query Match 1.4%; Score 24; DB 5; Length 464;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACCTCGCGCGGACCGC 1713
DB 30 TAAGTACCTCGCGCGGACCGC 7
RESULT 92
ADI76923/c
ID ADI76923 standard; DNA; 464 BP.
XX
XX ADI76923;
XX
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #9665.
XX

KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

OS Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-0207124P.

PR 15-JUN-2000; 2000US-0211940P.

PR 07-JUL-2000; 2000US-0216820P.

PR 25-JUL-2000; 2000US-0220661P.

PR 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian

XX cancer cells as compared to their normal non-cancerous ovarian cells are

XX used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 9665; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in

XX ovarian cancer cells as compared to their expression in normal (i.e. non-

XX cancerous) ovarian cells. The invention also relates to polypeptides

XX encoded by the markers, antibodies that selectively bind to the

XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk

XX of developing ovarian cancer involving inhibiting expression of a gene

XX corresponding to a marker of the invention and a method of treating a

XX patient afflicted with ovarian cancer comprising providing to cells of

XX the patient an antisense oligonucleotide complementary to a marker of the

XX invention. The markers are useful for assessing if a patient is afflicted

XX with ovarian cancer, which involves comparing the level of expression of

XX a marker in a patient sample and a normal level of expression of the

XX marker in a control non-ovarian cancer sample. A difference between the

XX expression levels indicates ovarian cancer. The level of expression of a

XX marker corresponds to a secreted protein or to a transcribed

XX polynucleotide or its portion. The level of expression of the marker is

XX assessed by detecting the presence in the sample, a protein or protein

XX fragment corresponding to the marker. The presence of protein or protein

XX protein is detected using an antibody that specifically binds with the

XX the marker is assessed by detecting the presence of a transcribed

XX polynucleotide which anneals with the marker or anneals with a portion of

XX the polynucleotide comprising the marker, under stringent conditions. The

XX marker is also used for monitoring the progression of ovarian cancer in a

XX patient which involves detecting expression of the marker in a patient

XX sample at a first point in time, repeating the method at a subsequent

XX time and comparing the level of expression. The method is carried out

XX using an ovarian tissue sample. A composition comprising a marker,

XX polypeptide or antibody of the invention is used to treat ovarian cancer.

XX This sequence represents a human ovarian cancer DNA marker of the

XX invention. Note: The sequence data for this patent did not form part of

XX the printed specification, but was obtained in electronic format directly

XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 464 BP; 146 A; 91 C; 92 G; 116 T; 0 U; 19 Other;

XX Query Match 1.4%; Score 24; DB 5; Length 464;

XX Best Local Similarity 100.0%; Pred. No. 1;

XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACACGC 1713

Db 30 TAAGTACTCGCGCGGACACGC 7

RESULT 93

ADL41961/c

ID ADL41961 standard; DNA; 471 BP.

XX ADL41961;

XX 20-MAY-2004 (first entry)

XX Human ovarian cancer DNA marker #15851.

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-0207124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

XX 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian

XX cancer cells as compared to their normal non-cancerous ovarian cells are

XX used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 15851; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in

XX ovarian cancer cells as compared to their expression in normal (i.e. non-

XX cancerous) ovarian cells. The invention also relates to polypeptides

XX encoded by the markers, antibodies that selectively bind to the

XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk

XX of developing ovarian cancer involving inhibiting expression of a gene

XX corresponding to a marker of the invention and a method of treating a

XX patient afflicted with ovarian cancer comprising providing to cells of

XX the patient an antisense oligonucleotide complementary to a marker of the

XX invention. The markers are useful for assessing if a patient is afflicted

XX with ovarian cancer, which involves comparing the level of expression of

XX a marker in a patient sample and a normal level of expression of the

XX marker in a control non-ovarian cancer sample. A difference between the

XX expression levels indicates ovarian cancer. The level of expression of a

XX marker corresponds to a secreted protein or to a transcribed

XX polynucleotide or its portion. The level of expression of the marker is

XX assessed by detecting the presence in the sample, a protein or protein

XX fragment corresponding to the marker. The presence of protein or protein

XX fragment is detected using an antibody that specifically binds with the

XX protein or protein fragment. Alternatively, the level of expression of

XX the marker is assessed by detecting the presence of a transcribed

XX polynucleotide which anneals with the marker or anneals with a portion of

XX the polynucleotide comprising the marker, under stringent conditions. The

XX marker is also used for monitoring the progression of ovarian cancer in a

XX patient which involves detecting expression of the marker in a patient

XX sample at a first point in time, repeating the method at a subsequent

XX time and comparing the level of expression. The method is carried out

XX using an ovarian tissue sample. A composition comprising a marker,

XX polypeptide or antibody of the invention is used to treat ovarian cancer.

XX This sequence represents a human ovarian cancer DNA marker of the

XX invention. Note: The sequence data for this patent did not form part of

XX the printed specification, but was obtained in electronic format directly

XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 471 BP; 132 A; 68 C; 104 G; 167 T; 0 U; 0 Other;
SQ Query Match 1.4%; Score 24; DB 5; Length 471;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCTGGCGCGACCGC 1713
Db 103 TAAGTACTCTGGCGCGACCGC 80

RESULT 94
ADL36885/c
ID ADL36885 standard; DNA; 486 BP.
XX AC ADL36885;
XX DT 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #10775.
XX DE Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX KW Homo sapiens.
XX OS Homo sapiens.
XX PN WO200170979-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009126.
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PA Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
XX PS Disclosure; SEQ ID NO 10775; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of

CC the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. CC This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 486 BP; 177 A; 69 C; 86 G; 135 T; 0 U; 19 Other;
Query Match 1.4%; Score 24; DB 5; Length 486;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCTGGCGCGACCGC 1713
Db 30 TAAGTACTCTGGCGCGACCGC 7

RESULT 95
ADI71730/c
ID ADI71730 standard; DNA; 486 BP.
XX AC ADI71730;
XX DT 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #4472.
XX DE Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX KW Homo sapiens.
XX OS Homo sapiens.
XX PN WO200170979-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009126.
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PA Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
XX PS Disclosure; SEQ ID NO 4472; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of

CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX SQ Sequence 486 BP; 177 A; 69 C; 86 G; 135 T; 0 U; 19 Other;
Query Match 1.4%; Score 24; DB 5; Length 486;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAACTACTCTCGCGCGACACGCG 1713
DB 30 TAACTACTCTCGCGCGACACGCG 7

RESULT 96
AAH69562/C
ID AAH69562 standard; cDNA; 500 BP.
XX AC AAH69562;
XX 19-SEP-2001 (first entry)
XX Human cervical cancer marker nucleic acid 836.
DE Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX Homo sapiens.
XX WO200142467-A2.
XX 14-JUN-2001.

XX 08-DEC-2000; 2000WO-US033312.
XX 08-DEC-1999; 99US-0169681P.
PR 21-DEC-1999; 99US-0171350P.
PR 14-MAR-2000; 2000US-0189315P.
PR 12-MAY-2000; 2000US-0203791P.
PR 09-JUN-2000; 2000US-0210600P.
PR 21-JUL-2000; 2000US-0220114P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Deeds J, Berger A, Zhao X;
PI WPI; 2001-375006/39.
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
XX for assessing and detecting compounds for treating the cancer.
XX Claim 1; Page 244-245; 1051pp; English.

XX The invention relates to novel genes (AAH68727-AAH73383) associated with
XX cervical cancer with cytostatic activity. The nucleic acids and encoded
XX polypeptides are useful: to assess if a patient is afflicted with

CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
XX useful for gene therapy

SQ Sequence 500 BP; 145 A; 108 C; 99 G; 148 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAACTACTCTCGCGCGACACGCG 1713
DB 30 TAACTACTCTCGCGCGACACGCG 7

RESULT 97
ADL42477/C
ID ADL42477 standard; DNA; 503 BP.
XX AC ADL42477;
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #16367.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.
XX 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Illie J;
PI WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 16367; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein

CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 503 BP; 166 A; 92 C; 74 G; 170 T; 0 U; 1 Other;

Query Match 1.4%; Score 24; DB 5; Length 503;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCTCGCGCGACACGC 1713

DB 85 TAACTACTCTCGCGCGACACGC 62

RESULT 98

ADL42086/c

ID ADL42086 standard; DNA; 517 BP.

XX

AC ADL42086;

DT 20-MAY-2004 (first entry)

DE Human ovarian cancer DNA marker #15976.

KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

OS Homo sapiens.

PN WO200170979-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US009126.

PR 21-MAR-2000; 2000US-0191031P.

PR 25-MAY-2000; 2000US-0207124P.

PR 15-JUN-2000; 2000US-0211940P.

PR 07-JUL-2000; 2000US-0216820P.

PR 25-JUL-2000; 2000US-0220661P.

PR 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

DR Novel isolated nucleic acid molecules (markers) overexpressed in ovarian

XX cancer cells as compared to their normal non-cancerous ovarian cells are

XX used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 15976; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene

CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX SQ Sequence 517 BP; 145 A; 76 C; 111 G; 185 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 517;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCTCGCGCGACACGC 1713

DB 102 TAACTACTCTCGCGCGACACGC 79

RESULT 99

AD172251/c

ID AD172251 standard; DNA; 521 BP.

XX

AC AD172251;

DT 20-MAY-2004 (first entry)

DE Human ovarian cancer DNA marker #4993.

KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

OS Homo sapiens.

PN WO200170979-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US009126.

PR 21-MAR-2000; 2000US-0191031P.

PR 25-MAY-2000; 2000US-0207124P.

PR 15-JUN-2000; 2000US-0211940P.

PR 07-JUL-2000; 2000US-0216820P.

PR 25-JUL-2000; 2000US-0220661P.

PR 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian

XX cancer cells as compared to their normal non-cancerous ovarian cells are

XX used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 4993; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in

XX ovarian cancer cells as compared to their expression in normal (i.e. non-

XX cancerous) ovarian cells. The invention also relates to polypeptides

XX encoded by the markers, antibodies that selectively bind to the

XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk

XX of developing ovarian cancer involving inhibiting expression of a gene

XX corresponding to a marker of the invention and a method of treating a

XX patient afflicted with ovarian cancer comprising providing to cells of

XX the patient an antisense oligonucleotide complementary to a marker of the

XX invention. The markers are useful for assessing if a patient is afflicted

XX with ovarian cancer, which involves comparing the level of expression of

XX a marker in a patient sample and a normal level of expression of the

XX marker in a control non-ovarian cancer sample. A difference between the

XX expression levels indicates ovarian cancer. The level of expression of a

XX marker corresponds to a secreted protein or to a transcribed

XX polynucleotide or its portion. The level of expression of the marker is

XX assessed by detecting the presence in the sample, a protein or protein

XX fragment corresponding to the marker. The presence of protein or protein

XX fragment is detected using an antibody that specifically binds with the

XX protein or protein fragment. Alternatively, the level of expression of

XX the marker is assessed by detecting the presence of a transcribed

XX polynucleotide which anneals with the marker or anneals with a portion of

XX the polynucleotide comprising the marker, under stringent conditions. The

XX marker is also used for monitoring the progression of ovarian cancer in a

XX patient which involves detecting expression of the marker in a patient

XX sample at a first point in time, repeating the method at a subsequent

XX time and comparing the level of expression. The method is carried out

XX using an ovarian tissue sample. A composition comprising a marker,

XX polypeptide or antibody of the invention is used to treat ovarian cancer.

XX This sequence represents a human ovarian cancer DNA marker of the

XX invention. Note: The sequence data for this patent did not form part of

XX the printed specification, but was obtained in electronic format directly

XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 521 BP; 110 A; 132 C; 124 G; 153 T; 0 U; 2 Other;

Query Match 1.4%; Score 24; DB 5; Length 521;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713

Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 100

ADL41725/c

ID ADL41725 standard; DNA; 521 BP.

XX AC ADL41725;

XX 20-MAY-2004 (first entry)

XX Human ovarian cancer DNA marker #15615.

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-0207124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

PR 21-DEC-2000; 2000US-0257672P.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian

XX cancer cells as compared to their normal non-cancerous ovarian cells are

XX used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 15615; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in

XX ovarian cancer cells as compared to their expression in normal (i.e. non-

XX cancerous) ovarian cells. The invention also relates to polypeptides

XX encoded by the markers, antibodies that selectively bind to the

XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk

XX of developing ovarian cancer involving inhibiting expression of a gene

XX corresponding to a marker of the invention and a method of treating a

XX patient afflicted with ovarian cancer comprising providing to cells of

XX the patient an antisense oligonucleotide complementary to a marker of the

XX invention. The markers are useful for assessing if a patient is afflicted

XX with ovarian cancer, which involves comparing the level of expression of

XX a marker in a patient sample and a normal level of expression of the

XX marker in a control non-ovarian cancer sample. A difference between the

XX expression levels indicates ovarian cancer. The level of expression of a

XX marker corresponds to a secreted protein or to a transcribed

XX polynucleotide or its portion. The level of expression of the marker is

XX assessed by detecting the presence in the sample, a protein or protein

XX fragment corresponding to the marker. The presence of protein or protein

XX fragment is detected using an antibody that specifically binds with the

XX protein or protein fragment. Alternatively, the level of expression of

XX the marker is assessed by detecting the presence of a transcribed

XX polynucleotide which anneals with the marker or anneals with a portion of

XX the polynucleotide comprising the marker, under stringent conditions. The

XX marker is also used for monitoring the progression of ovarian cancer in a

XX patient which involves detecting expression of the marker in a patient

XX sample at a first point in time, repeating the method at a subsequent

XX time and comparing the level of expression. The method is carried out

XX using an ovarian tissue sample. A composition comprising a marker,

XX polypeptide or antibody of the invention is used to treat ovarian cancer.

XX This sequence represents a human ovarian cancer DNA marker of the

XX invention. Note: The sequence data for this patent did not form part of

XX the printed specification, but was obtained in electronic format directly

XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 521 BP; 214 A; 69 C; 88 G; 150 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 521;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713

Db 106 TAAGTACTCGCGCGACACGC 83

Search completed: March 11, 2006, 20:34:15

Job time : 1079 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 20:16:33 ; Search time 6306 Seconds
(without alignments)
12709.526 Million cell updates/sec

Title: US-09-989-890-105
Perfect score: 1713
Sequence: 1 agccccgcctggacaccc.....tacctggcgagaccacgc 1713

Scoring-table: OLIGO-NUC

Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word-size: 0
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hic:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gsa1:
10: gb_gsa2:
11: gb_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1361	79.5	1671	4	CR749558
2	1197	69.9	1197	11	DQ045548 Homo sapi
3	752	43.9	975	3	BM460277
4	635	37.1	917	5	BQ691555
5	622	36.3	622	3	BM823479 K-EST0094
6	598	34.9	753	7	CN289134 170005999
7	528	30.8	582	3	BP315176 BP315176
8	510	29.8	510	1	AA316608 EST188290
9	491	28.7	1181	11	DQ045549
10	480	28.0	489	1	AI925416
11	450	26.3	470	5	BE110746
12	450	26.3	966	2	BE901537
13	424	24.8	583	3	BP315124
14	370	21.6	370	1	AW589267
15	323	18.9	513	6	CD702656
16	321	18.7	330	1	AI702452
17	303	17.7	1015	2	BE741035
18	291	17.0	556	1	AA573775
19	244	14.2	412	1	AI216202
20	215	12.6	423	1	AW08047
21	213	12.4	244	2	BE162756
22	208	12.1	246	3	BM750392

96	26	1.5	707	8	CV943849	PU003E7.m	169	24	1.4	169	1	AW070076	AW070076 mgie1004D
97	26	1.5	722	3	BI409054	602961119	C 170	24	1.4	170	6	CA747328	CA747328 wri2s.pk0
98	26	1.5	737	3	CV944323	PU011H10	171	24	1.4	171	8	CV972003	CV972003 LRRG0200
99	26	1.5	746	2	BI159562	602919525	172	24	1.4	171	8	CV972495	CV972495 LRRG0249
100	26	1.5	746	3	BI905713	603166180	C 173	24	1.4	172	1	AJ747735	AJ747735 AJ747735
101	26	1.5	746	3	BI905189	603167516	174	24	1.4	177	8	CV971679	CV971679 LRRG0167
102	26	1.5	1040	3	BI411303	602964692	175	24	1.4	179	6	CF074335	CF074335 QAE45a02.
103	25	1.5	66	6	CF044340	QJ28f03.	176	24	1.4	180	6	CF044293	CF044293 QJ28a01.
104	25	1.5	91	6	CF051221	QCM22g08.	C 177	24	1.4	185	8	CV973009	CV973009 LRRG0300
105	25	1.5	216	7	CO499243	G.h.fbr-s	C 178	24	1.4	187	6	CA737687	CA737687 wpi2s.pk0
106	25	1.5	238	6	CA744277	wri1s.pk0	179	24	1.4	188	8	CA737687	CA737687 wpi2s.pk0
107	25	1.5	240	6	CA735724	wpi1s.pk0	C 180	24	1.4	195	8	CV971813	CV971813 LRRG0181
108	25	1.5	243	6	CA725861	wet1s.pk0	C 181	24	1.4	198	1	AL718125	AL718125 AL718125
109	25	1.5	256	1	AL717284	AL717284	C 182	24	1.4	199	1	AL716972	AL716972 AL716972
110	25	1.5	277	6	CA738002	wpi2s.pk0	183	24	1.4	199	1	AL727181	AL727181 AL727181
111	25	1.5	279	1	AB178686	AB178686	184	24	1.4	199	7	CF935254	CF935254 TE5E-B39
112	25	1.5	279	8	DR831531	MM18 So:g	185	24	1.4	199	8	CV888725	CV888725 LRRG0061
113	25	1.5	297	6	CB701477	AMGNUC:S	186	24	1.4	199	8	CV971800	CV971800 LRRG0179
114	25	1.5	298	6	CF036352	QCG30b12.	187	24	1.4	203	8	CV972977	CV972977 LRRG0297
115	25	1.5	307	6	CB697651	AMGNUC:S	188	24	1.4	203	8	DN911048	DN911048 DB35 Dire
116	25	1.5	310	1	AL717034	AL717034	C 189	24	1.4	204	8	CV971782	CV971782 LRRG0178
117	25	1.5	317	1	AB178706	AB178706	C 190	24	1.4	205	8	CV971708	CV971708 LRRG0170
118	25	1.5	322	6	CA737530	wpi2s.pk0	C 191	24	1.4	205	8	CV971759	CV971759 LRRG0175
119	25	1.5	322	6	CA737904	wpi2s.pk0	C 192	24	1.4	205	8	CV971786	CV971786 LRRG0178
120	25	1.5	322	6	CA737903	wpi2s.pk0	193	24	1.4	205	8	CV971804	CV971804 LRRG0180
121	25	1.5	324	6	CD988066	QAO8d11.y	C 194	24	1.4	206	8	CV971627	CV971627 LRRG0162
122	25	1.5	324	6	CD988141	QAO9402.y	C 195	24	1.4	206	8	CV971674	CV971674 LRRG0167
123	25	1.5	334	6	CA739700	wpi2s.pk0	C 196	24	1.4	207	8	CV971796	CV971796 LRRG0179
124	25	1.5	360	6	CA734859	wpi1s.pk0	C 197	24	1.4	207	8	CV971838	CV971838 LRRG0183
125	25	1.5	389	1	AJ574663	AJ574663	C 198	24	1.4	208	1	AJ311285	AJ311285 AL711285
126	25	1.5	396	6	CA739569	wpi2s.pk0	199	24	1.4	209	1	AJ603463	AJ603463 AJ603463
127	25	1.5	398	6	CA737872	wpi2s.pk0	200	24	1.4	214	8	CV888396	CV888396 LRRG0028
128	25	1.5	401	6	CA738547	wpi2s.pk0	C 201	24	1.4	214	8	CV971688	CV971688 LRRG0168
129	25	1.5	424	6	CA747337	wri2s.pk0	C 202	24	1.4	216	6	CD987884	CD987884 QAO6b12.y
130	25	1.5	438	7	CO495035	G.h.fbr-s	C 203	24	1.4	220	8	CV888809	CV888809 LRRG0070
131	25	1.5	441	6	CD988054	QAO8c05.y	C 204	24	1.4	221	8	CV971801	CV971801 LRRG0180
132	25	1.5	443	7	CO491121	G.h.fbr-s	205	24	1.4	223	8	CV888694	CV888694 LRRG0058
133	25	1.5	448	7	CO496357	G.h.fbr-s	C 206	24	1.4	224	8	CV888788	CV888788 LRRG0067
134	25	1.5	456	1	AL723103	AL723103	C 207	24	1.4	225	6	CF049222	CF049222 QCL32g08.
135	25	1.5	500	8	CM067388	1322678.N	C 208	24	1.4	226	6	CV888412	CV888412 LRRG0030
136	25	1.5	518	8	CM067821	1322679.N	C 209	24	1.4	228	8	CV888718	CV888718 LRRG0060
137	25	1.5	519	8	CM066860	1321003.N	C 210	24	1.4	228	8	CV972485	CV972485 LRRG0248
138	25	1.5	523	8	CM066859	1321002.N	C 211	24	1.4	230	1	AJ311187	AJ311187 AL711187
139	25	1.5	533	1	AL728024	AL728024	212	24	1.4	230	6	CF031884	CF031884 OCE10h05.
140	25	1.5	564	1	AL730200	AL730200	C 213	24	1.4	231	8	CV888765	CV888765 LRRG0065
141	25	1.5	566	6	CF039408	QCH36C01.	214	24	1.4	231	6	CA737821	CA737821 wpi2s.pk0
142	25	1.5	583	1	AL730528	AL730528	215	24	1.4	232	6	CA738152	CA738152 wpi2s.pk0
143	25	1.5	626	7	CO499053	G.h.fbr-s	216	24	1.4	232	6	CA738581	CA738581 wpi2s.pk0
144	25	1.5	640	1	AJ747135	AJ747135	217	24	1.4	232	6	CV971598	CV971598 LRRG0159
145	25	1.5	653	8	DN479092	alt013x0	C 218	24	1.4	232	8	CV971769	CV971769 LRRG0176
146	25	1.5	655	7	CO498240	G.h.fbr-s	C 219	24	1.4	232	8	CV972387	CV972387 LRRG0238
147	25	1.5	712	1	AL726657	AL726657	C 220	24	1.4	234	8	CV888729	CV888729 LRRG0062
148	25	1.5	727	1	AL723924	AL723924	C 221	24	1.4	235	6	CV888729	CV888729 LRRG0062
149	25	1.5	749	1	AL717219	AL717219	222	24	1.4	236	6	CA739858	CA739858 wpi2s.pk0
150	25	1.5	751	8	CV944783	PU023B08	223	24	1.4	236	8	CV972472	CV972472 LRRG0247
151	25	1.5	757	1	AL728866	AL728866	C 224	24	1.4	237	6	CA737696	CA737696 wpi2s.pk0
152	25	1.5	769	7	CK473171	AGENCYCOURT	C 225	24	1.4	237	6	CA738286	CA738286 wpi2s.pk0
153	25	1.5	783	7	CK478920	AGENCYCOURT	C 226	24	1.4	237	6	CA738801	CA738801 wpi2s.pk0
154	25	1.5	815	8	CV943874	PU004B1.m	C 227	24	1.4	237	6	CA739443	CA739443 wpi2s.pk0
155	25	1.5	825	8	DN936585	AGENCYCOURT	C 228	24	1.4	237	7	CF922018	CF922018 gmrHrw24
156	25	1.5	841	8	DN479809	alt016xm	229	24	1.4	237	7	CF922018	CF922018 gmrHrw24
157	24	1.4	112	1	AL715946	alt015946	C 230	24	1.4	237	8	CV972479	CV972479 LRRG0247
158	24	1.4	116	6	CF063067	QCU17b01.	C 231	24	1.4	239	8	CV888588	CV888588 LRRG0047
159	24	1.4	140	6	CD974935	QAE51d04.	C 232	24	1.4	239	8	CV888588	CV888588 LRRG0054
160	24	1.4	142	8	CK127407	laccST 14	C 233	24	1.4	241	8	CV888716	CV888716 LRRG0060
161	24	1.4	147	1	AI267176	aq36f01.x	C 234	24	1.4	241	8	CV972362	CV972362 LRRG0236
162	24	1.4	149	7	CV699598	PJS-177-T	C 235	24	1.4	242	6	CF032278	CF032278 OCE15g03.
163	24	1.4	151	6	CF048886	QCL28g08.	C 236	24	1.4	244	1	AW069912	AW069912 mgie1001C
164	24	1.4	152	8	CK127132	laccST 12	C 237	24	1.4	244	6	CF049480	CF049480 QCL37a10.
165	24	1.4	152	8	CK127618	laccST 17	C 238	24	1.4	245	2	BG833709	BG833709 EST0015.H
166	24	1.4	159	1	AL726990	AL726990	C 239	24	1.4	246	8	CV972353	CV972353 LRRG0235
167	24	1.4	160	1	AL717654	AL717654	240	24	1.4	247	1	AL714471	AL714471 AL714471
168	24	1.4	160	6	CF044444	QCU29h12.	C 241	24	1.4	247	8	CV888738	CV888738 LRRG0062

C 242	24	1.4	247	8	CV971662	CV971662 LRRGE0166	315	24	1.4	313	6	CA743121	CA743121 wr118.pk0
C 243	24	1.4	247	8	CV972951	CV972951 LRRGE0295	316	24	1.4	313	6	CF054443	CF054443 QCN296004
C 244	24	1.4	248	8	CV971863	CV971863 LRRGE0186	C 317	24	1.4	314	6	CF061027	CF061027 QCN16508
C 245	24	1.4	249	8	CV888563	CV888563 LRRGE0045	C 318	24	1.4	318	1	AL727194	AL727194 AMGNNUC:S
C 246	24	1.4	250	8	CV971789	CV971789 LRRGE0178	C 319	24	1.4	318	6	CB708394	CB708394 AMGNNUC:S
C 247	24	1.4	250	8	CV972906	CV972906 LRRGE0290	C 320	24	1.4	318	6	CF048958	CF048958 QCN29005
C 248	24	1.4	251	6	CD987982	CD987982 QAO7D08.Y	C 321	24	1.4	318	6	CF053993	CF053993 QCN23602
C 249	24	1.4	251	8	CV972378	CV972378 LRRGE0237	C 322	24	1.4	320	6	CA737943	CA737943 wp128.pk0
C 250	24	1.4	253	8	CV972487	CV972487 LRRGE0248	C 323	24	1.4	320	6	CA738263	CA738263 wr128.pk0
C 251	24	1.4	254	6	CF064071	CF064071 QCU6H04.Y	C 324	24	1.4	324	1	AJ746964	AJ746964
C 252	24	1.4	254	8	CV888898	CV888898 LRRGE0078	C 325	24	1.4	325	6	CF046938	CF046938 QCK31G05
C 253	24	1.4	256	8	CV972340	CV972340 LRRGE0234	C 326	24	1.4	326	1	AL729207	AL729207 QCK31G05
C 254	24	1.4	256	8	CV972386	CV972386 LRRGE0238	C 327	24	1.4	327	1	AJ746818	AJ746818
C 255	24	1.4	259	5	BQ73282	BQ73282 ubel-47.P	C 328	24	1.4	327	1	AJ746823	AJ746823
C 256	24	1.4	259	6	CF062729	CF062729 QCU12H10	C 329	24	1.4	330	8	CV972998	CV972998 LRRGE0299
C 257	24	1.4	259	8	CV972010	CV972010 LRRGE0201	C 330	24	1.4	331	1	AW682514	AW682514 EST01363
C 258	24	1.4	263	8	CV971625	CV971625 LRRGE0162	C 331	24	1.4	332	8	CV972936	CV972936 LRRGE0293
C 259	24	1.4	268	8	CV971941	CV971941 LRRGE0194	C 332	24	1.4	333	8	CV888589	CV888589 LRRGE0048
C 260	24	1.4	269	6	CA745301	CA745301 wr118.pk0	C 333	24	1.4	336	6	CA736806	CA736806 wp118.pk0
C 261	24	1.4	270	1	AL718701	AL718701	C 334	24	1.4	337	6	CF800490	CF800490 EST0011.M
C 262	24	1.4	270	6	CF053980	CF053980 QCN23C10	C 335	24	1.4	337	6	CF800550	CF800550 EST0071.M
C 263	24	1.4	270	6	CF054088	CF054088 QCN24G10	C 336	24	1.4	340	6	CB694231	CB694231 AMGNNUC:S
C 264	24	1.4	270	6	CF054150	CF054150 QCN25607	C 337	24	1.4	341	6	CB693915	CB693915 AMGNNUC:S
C 265	24	1.4	270	6	CF054174	CF054174 QCN25610	C 338	24	1.4	341	8	CV888459	CV888459 LRRGE0035
C 266	24	1.4	270	6	CF054270	CF054270 QCN27D12	C 339	24	1.4	341	8	CV888866	CV888866 LRRGE0075
C 267	24	1.4	270	6	CF054429	CF054429 QCN29C08	C 340	24	1.4	343	1	AL727759	AL727759
C 268	24	1.4	270	6	CF054694	CF054694 QCN31G06	C 341	24	1.4	344	8	CV972098	CV972098 LRRGE0209
C 269	24	1.4	270	8	CV971702	CV971702 LRRGE0170	C 342	24	1.4	346	8	CV888613	CV888613 LRRGE0050
C 270	24	1.4	273	8	CV888789	CV888789 LRRGE0068	C 343	24	1.4	346	8	CV888754	CV888754 LRRGE0064
C 271	24	1.4	276	6	CA743006	CA743006 wr118.pk0	C 344	24	1.4	353	6	CA736644	CA736644 wp118.pk0
C 272	24	1.4	276	6	CF053969	CF053969 QCN23D05	C 345	24	1.4	353	8	DN976310	DN976310 Gp_masB.0
C 273	24	1.4	277	6	CF051228	CF051228 QCN22H08	C 346	24	1.4	354	6	CA736245	CA736245 wp118.pk0
C 274	24	1.4	277	7	CN121113	CN121113 EST122-C0	C 347	24	1.4	354	6	CA736685	CA736685 wp118.pk0
C 275	24	1.4	280	6	CA735250	CA735250 wp118.pk0	C 348	24	1.4	355	6	CA736939	CA736939 wp118.pk0
C 276	24	1.4	282	5	BQ580373	BQ580373 EST-SF-00	C 349	24	1.4	357	7	CO499783	CO499783 G.h.fbr-s
C 277	24	1.4	282	6	CA735019	CA735019 wp118.pk0	C 350	24	1.4	357	8	CO568105	CO568105 1322922.N
C 278	24	1.4	284	8	CV972179	CV972179 LRRGE0217	C 351	24	1.4	358	8	CV972089	CV972089 LRRGE0208
C 279	24	1.4	285	1	AL725508	AL725508 LRRGE0217	C 352	24	1.4	359	6	CF800528	CF800528 EST0049.M
C 280	24	1.4	285	8	CV972930	CV972930 LRRGE0293	C 353	24	1.4	360	6	CA736173	CA736173 wp118.pk0
C 281	24	1.4	286	6	CB711104	CB711104 AMGNNUC:S	C 354	24	1.4	360	6	CA744861	CA744861 wr118.pk0
C 282	24	1.4	287	1	AL723262	AL723262	C 355	24	1.4	360	6	CA744861	CA744861 wr118.pk0
C 283	24	1.4	287	7	CO494502	CO494502 G.h.fbr-s	C 356	24	1.4	360	7	CV186322	CV186322 Lr.RS1CF
C 284	24	1.4	288	6	CF054710	CF054710 QCN31H12	C 357	24	1.4	361	8	DN911004	DN911004 C745.Supp
C 285	24	1.4	288	8	CV972797	CV972797 LRRGE0279	C 358	24	1.4	362	1	AL714499	AL714499
C 286	24	1.4	289	1	AA933277	AA933277 SWBML3SA4	C 359	24	1.4	362	6	CA735367	CA735367 wp118.pk0
C 287	24	1.4	289	1	AL726365	AL726365	C 360	24	1.4	363	6	CA735376	CA735376 wp118.pk0
C 288	24	1.4	289	1	AL731019	AL731019	C 361	24	1.4	363	6	CA736942	CA736942 wp118.pk0
C 289	24	1.4	289	7	CO491636	CO491636 G.h.fbr-s	C 362	24	1.4	363	6	CA737006	CA737006 LRRGE0300
C 290	24	1.4	292	6	CF054920	CF054920 QCN34F11	C 363	24	1.4	366	6	CA735476	CA735476 wp118.pk0
C 291	24	1.4	292	6	CF055046	CF055046 QCN36C10	C 364	24	1.4	366	6	CA742463	CA742463 wr118.pk0
C 292	24	1.4	292	6	CF062732	CF062732 QCU13A03	C 365	24	1.4	367	6	CA743232	CA743232 wr118.pk0
C 293	24	1.4	294	8	CV972830	CV972830 LRRGE0283	C 366	24	1.4	369	6	CF056835	CF056835 QCO24C10
C 294	24	1.4	294	8	CK066675	CK066675 1320936.N	C 367	24	1.4	370	6	CD051308	CD051308 EST0657.S
C 295	24	1.4	296	6	CF061287	CF061287 QCT19H05	C 368	24	1.4	371	8	CV972607	CV972607 LRRGE0260
C 296	24	1.4	300	1	AW681436	AW681436 EST00154	C 369	24	1.4	373	1	AL726483	AL726483
C 297	24	1.4	300	8	CV972382	CV972382 LRRGE0238	C 370	24	1.4	375	1	A1079069	A1079069 SWBML3SBH
C 298	24	1.4	301	8	AL722665	AL722665 LRRGE0266	C 371	24	1.4	376	6	CA735131	CA735131 wp118.pk0
C 299	24	1.4	302	1	AL722343	AL722343	C 372	24	1.4	377	1	AW682168	AW682168 EST00935
C 300	24	1.4	302	1	AW681908	AW681908 EST00626	C 373	24	1.4	381	1	AL717711	AL717711
C 301	24	1.4	303	1	AW681753	AW681753 EST00471	C 374	24	1.4	381	6	CF059676	CF059676 QCS15C11
C 302	24	1.4	303	8	CK125995	CK125995 gamBST.80	C 375	24	1.4	381	6	CF569158	CF569158 EST019.Su
C 303	24	1.4	304	7	CO497484	CO497484 G.h.fbr-s	C 376	24	1.4	382	8	CV888255	CV888255 LRRGE0014
C 304	24	1.4	304	8	CK943962	CK943962 DH0AGB122	C 377	24	1.4	382	8	CV888437	CV888437 LRRGE0032
C 305	24	1.4	306	7	CK928056	CK928056 haap006xk	C 378	24	1.4	384	7	CV700372	CV700372 PJS-08-H0
C 306	24	1.4	306	8	CV972623	CV972623 LRRGE0262	C 379	24	1.4	385	1	AJ568378	AJ568378
C 307	24	1.4	310	1	AL723307	AL723307	C 380	24	1.4	385	1	AL715610	AL715610
C 308	24	1.4	310	6	CB697136	CB697136 AMGNNUC:S	C 381	24	1.4	387	7	CF922789	CF922789 gmchrwv24
C 309	24	1.4	310	8	CV972856	CV972856 LRRGE0285	C 382	24	1.4	387	7	CV700192	CV700192 PJS-06-E0
C 310	24	1.4	311	1	AW681485	AW681485 EST00203	C 383	24	1.4	388	1	AL715913	AL715913
C 311	24	1.4	311	6	CB696756	CB696756 AMGNNUC:S	C 384	24	1.4	390	8	CV972915	CV972915 LRRGE0291
C 312	24	1.4	311	7	CO494812	CO494812 G.h.fbr-s	C 385	24	1.4	392	6	CA746361	CA746361 wr128.pk0
C 313	24	1.4	311	7	CO495865	CO495865 G.h.fbr-s	C 386	24	1.4	393	7	CO497659	CO497659 G.h.fbr-s
C 314	24	1.4	312	7	CO493506	CO493506 G.h.fbr-s	C 387	24	1.4	393	8	CV972911	CV972911 LRRGE0291

C 388	24	1.4	394	8	CV888266	CV888266	LRRGB0015	C 461	24	1.4	510	1	AL725812	AL725812
C 389	24	1.4	395	1	AW681360	EST00078	AW681360	C 462	24	1.4	515	7	CN852426	H20 Healt
C 390	24	1.4	396	6	CB707964	ANGNNUC:S	CB707964	C 463	24	1.4	516	6	CF039158	QCH32f10
C 391	24	1.4	400	8	CV971920	LRRGB0191	CV971920	C 464	24	1.4	517	6	CF062230	QCT6903.y
C 392	24	1.4	402	6	CB769571	ANGNNUC:M	CB769571	C 465	24	1.4	519	8	CV972855	LRRGB0265
C 393	24	1.4	403	6	CF063579	QCU23e02	CF063579	C 466	24	1.4	520	6	CB715612	CB715612
C 394	24	1.4	405	8	DN154781	3057_Xeno	DN154781	C 467	24	1.4	520	8	CF054336	OCN28a11
C 395	24	1.4	408	1	AL719074	AL719074	AL719074	C 468	24	1.4	520	8	CF054336	OCN28a11
C 396	24	1.4	408	6	CB770403	ANGNNUC:S	CB770403	C 469	24	1.4	521	6	CB720919	ANGNNUC:S
C 397	24	1.4	408	6	CB770406	ANGNNUC:S	CB770406	C 470	24	1.4	523	6	CA743604	CA743604
C 398	24	1.4	409	6	CF036166	QCG28d11	CF036166	C 471	24	1.4	523	6	CA743604	CA743604
C 399	24	1.4	414	7	CN072146	B327_Pax1	CN072146	C 472	24	1.4	523	6	CF060507	QCT10c09
C 400	24	1.4	417	6	CF049280	QCL33e08	CF049280	C 473	24	1.4	524	6	CF055192	QCN38c02
C 401	24	1.4	417	7	CO494143	G.h.fbr-s	CO494143	C 474	24	1.4	524	8	DR831489	MM5_Sorgh
C 402	24	1.4	418	6	CD975066	QAE53a07	CD975066	C 475	24	1.4	526	6	CF060513	QCT10d03
C 403	24	1.4	419	6	CB764922	ANGNNUC:N	CB764922	C 476	24	1.4	536	1	AW682236	EST01018
C 404	24	1.4	421	6	CB764383	ANGNNUC:S	CB764383	C 477	24	1.4	537	6	CF057554	QCO33e03
C 405	24	1.4	423	6	CA738150	wp128.pk0	CA738150	C 478	24	1.4	542	1	AL719579	AL719579
C 406	24	1.4	424	6	CB796120	ANGNNUC:S	CB796120	C 479	24	1.4	542	1	AL729401	AL729401
C 407	24	1.4	427	6	CA736482	wp1ls.pk0	CA736482	C 480	24	1.4	542	7	CV699731	PJS-303-T
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ALIGNMENTS

RESULT 1	CR749558	CR749558	1671 bp	mRNA	linear	HTC 19-AUG-2004
LOCUS	Homo sapiens	mRNA; cDNA	DKFZp686B17277	(from clone	DKFZp686B17277)	
DEFINITION	CR749558					
ACCESSION	CR749558.1	GI:51476784				
VERSION	HTC					
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 1671)					
AUTHORS	Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Newes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.					
CONSTRM	The German cDNA Consortium					
TITLE	Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764					
JOURNAL	Neuberberg, GERMANY					
COMMENT	Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686B17277) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneId=DKFZp686B17277					

Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

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Qy	396	TGAGTGTCCCCCCAGCCCTGATCTGTGCACCCCCAGCGCGGGGATGGCCAGCGGCTCAA	455	
Db	346	TGGAGTGTCCCCCCAGCCCTGATCTGTGCACCCCCAGCGCGGGGATGGCCAGCGGCTCAA	405	
Qy	456	GTCAACATGGGCGAGGAGCTTCAGGTACCCCGATGTTAAGCTCAAGGCGATCCCTGTGTGA	515	
Db	406	GTCAACATGGGCGAGGAGCTTCAGGTACCCCGATGTTAAGCTCAAGGCGATCCCTGTGTGA	465	
Qy	516	TCCCTACCCGAGGGGCCACCTCCCGAGCCCGTGTGCGGACTCTGTCTCAAGGAGGCCACT	575	
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Qy	576	GGCGGATCCCCCAACCCATGCGACACAGCGCTGCCGACGACCTTTGCGCAGTAGTCTCTCGTGG	635	
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Qy	636	CTCGGAGGAGTACTATTCTTTTCCATGAGTCTGGACCTGCGGAGATGGGCGAGTGG	695	
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Qy	696	CTCCATGTCTGAGCCGAGAAATTGATGTGCTCATCTTTCAAGAAGCTGCAGAGAGCTTTCAG	755	
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Qy	756	CGTACACAGATCGATGAGCTGGCCAAAGTGCACATCAGACACTGTGTTCCTGGAGAAAC	815	
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Qy	816	CAGTAAAGATCTCGGACCTTATCAGCAGGATCAGCGGAGCTACCACTCTGGATGACGAGA	875	
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ORIGIN

Query Match 43.9%; Score 752; DB 3; Length 975;
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Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 667 GACCTGACCTTCCGAGAGTGGGAGTGGCTCCATGTCGAGCGAGAAATGATGTGCTC 726
DB 61 GACCTGACCTTCCGAGAGTGGGAGTGGCTCCATGTCGAGCGAGAAATGATGTGCTC 120
QY 727 ATCTTCAAGAGTGCACAGAGTGTTCAGCGTACACAGATCGATGAGCTGGCCAAATGC 786
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QY 787 ACATCAGACACTGTGTCCTGGAGAGACCAAGTAAAGTCTCGACCTTATCAGCAGATC 846
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RESULT 4

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LOCUS BQ691555 917 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT 8341018 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6249453
5', mRNA sequence.
ACCESSION BQ691555
VERSION BQ691555.1 GI:21816871
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 917)

AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>
Plate: LCM2390 row: 0 column: 22
High quality sequence stop: 535.

FEATURES
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/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 37.1%; Score 635; DB 5; Length 917;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.D., Geoghegan, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y., Bednari, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
7566098

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
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VERSION DQ045549.1 GI:66896764
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 1181)
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civallo, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1181)
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civallo, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
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ORIGIN
    Query Match      28.7%; Score 491; DB 11; Length 1181;
    Best Local Similarity 99.8%; Pred. No. 9.6e-241;
    Matches 541; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 640 GAGGAGTACTATCTTTTCATGATCGGACCTGGACCTCCCGGAGATGGGAGTGGCTCC 699
Db 640 GAGGAGTACTATCTTTTCATGATCGGACCTGGACCTCCCGGAGATGGGAGTGGCTCC 699

QY 700 ATGTGCGAGCGGAGAAATTGATGTCTCATCTTCAAGAAGCTGACAGAGCTGTTTCACGGTA 759
Db 700 ATGTGCGAGCGGAGAAATTGATGTCTCATCTTCAAGAAGCTGACAGAGCTGTTTCACGGTA 759

QY 760 CACCAGATCGATGAGCTGGCCAAAGTGCAATCAGACACTGTGTCTTCTGGAGAGACAGT 819
Db 760 CACCAGATCGATGAGCTGGCCAAAGTGCAATCAGACACTGTGTCTTCTGGAGAGACAGT 819

QY 820 AAGATCTCGGACCTTATCATGACGACATCAGCAGGACTACACCTGGATGAGCAGGATGCT 879
Db 820 AAGATCTCGGACCTTATCATGACGACATCAGCAGGACTACACCTGGATGAGCAGGATGCT 879
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Db      820 AAGATCTCGGACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCT 879
Qy      880 GAGGCGCGCTGTGACCGCGCATCATTCGATAGTAGTACCCGAAAGACCGCTGTGCGCCA 939
Db      880 GAGGCGCGCTGTGACCGCGCATCATTCGATAGTAGTACCCGAAAGACCGCTGTGCGCCA 939
Qy      940 CAGACCTCGGAGGGTCTGCTCAACTCGGGCTGCTGCCCAACCCGCTGTGCGCCCTGACAGT 999
Db      940 CAGACCTCGGAGGGTCTGCTCAACTCGGGCTGCTGCCCAACCCGCTGTGCGCCCTGACAGT 999
Qy      1000 GGCCATGAGACCATGTGTGGGCTCAGGTCTCAGCCAGGATGAGTGCAGATGCACTCC 1059
Db      1000 GGCCATGAGACCATGTGTGGGCTCAGGTCTCAGCCAGGATGAGTGCAGATGCACTCC 1059
Qy      1060 CAGGAGACGACTGAGATGATCGCCCGAAGCTGAGGCTTATGAGTTCAGGCTAC 1119
Db      1060 CAGGAGACGACTGAGATGATCGCCCGAAGCTGAGGCTTATGAGTTCAGGCTAC 1119
Qy      1120 CCAGCAGGACCATGACTCATCTCCAGGCGCAGCAGACGACTCGTGGGGGACCCCTTG 1179
Db      1120 CCAGCAGGACCATGACTCATCTCCAGGCGCAGCAGACGACTCGTGGGGGACCCCTTG 1179
Qy      1180 CT 1181
Db      1180 CT 1181
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RESULT 10
AI925416/c
LOCUS   489 bp mRNA linear EST 08-MAR-2000
DEFINITION
wo30a02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2456810 3',
mRNA sequence.
VERSION
AI925416
GI:5661380
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 489)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@p5.kim.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 831 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 432.
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1..489
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2456810"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
/notes="NCI_CGAP Gas4"
/site="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
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ORIGIN

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Query Match 28.0%; Score 480; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.1e-235;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1217 CCACACCCCTTCTGGGAGAGCATGCGCTACAGAAATGAAGAGGGGACCAAGACCCCTG 1276
Db 489 CCACACCCCTTCTGGGAGAGCATGCGCTACAGAAATGAAGAGGGGACCAAGACCCCTG 430
Qy 1277 TGGGAGAGGCTTAGAGCTGAAGCAGTGCCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCT 1336
Db 429 TGGGAGAGGCTTAGAGCTGAAGCAGTGCCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCT 370
Qy 1337 GTTCTTGGACCATGTGCAATTTCACTGGGCCATGGATCTACATCTCTCTGCAATCCCGAC 1396
Db 369 GTTCTTGGACCATGTGCAATTTCACTGGGCCATGGATCTACATCTCTCTGCAATCCCGAC 310
Qy 1397 TGGTCTGATCCCTGCCAGGCGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1456
Db 309 TGGTCTGATCCCTGCCAGGCGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 250
Qy 1457 TGGAAAGTAAAGAGTAAAGCATTTACCTTCTGGGAGTGAACCCCTGACTCCATCCCTCTATT 1516
Db 249 TGGAAAGTAAAGAGTAAAGCATTTACCTTCTGGGAGTGAACCCCTGACTCCATCCCTCTATT 190
Qy 1517 GCCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAATTCACAGTTAAAGAA 1576
Db 189 GCCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAATTCACAGTTAAAGAA 130
Qy 1577 GCTTATCTTAAATGATTTATTTGGGGGTGGGCGAGGCCCACTCTATGTTATGTTAAGG 1636
Db 129 GCTTATCTTAAATGATTTATTTGGGGGTGGGCGAGGCCCACTCTATGTTATGTTAAGG 70
Qy 1637 AGTTGGTCTTGGTCTTGGCTGATGTTCTATCTTAAACATGACACAGTTTGTGAAGTAC 1696
Db 69 AGTTGGTCTTGGTCTTGGCTGATGTTCTATCTTAAACATGACACAGTTTGTGAAGTAC 10
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LOCUS   470 bp mRNA linear EST 07-FEB-2003
DEFINITION
BX110746 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:998E036110 ;
IMAGE:2456810, mRNA sequence.
VERSION
BX110746
GI:27836587
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 470)
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, J., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE:998E036110.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13u, Primer sequence: GTTGTAAACACGCGCCAGT.
Location/Qualifiers
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FEATURES


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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 583)
AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Institute of Virology
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ms.u-tokyo.ac.jp.
FEATURES
source
1. 583
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/db_xref="taxon:9606"
/clone="R0109504"
/tissue_type="rectum"
/clone_lib="Sugano cDNA library, rectum"
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Query Match 24.8%; Score 424; DB 3; Length 583;
Best Local Similarity 100.0%; Pred. No. 2.9e-206;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 76 TGTCTGAGACATATGATAAACCACCTCAGCCCCCAAGCCGCGCCAGCCGCTAGACCA 135
DB 59 TGTCTGAGACATATGATAAACCACCTCAGCCCCCAAGCCGCGCCAGCCGCTAGACCA 118
QY 136 GACCCCAAGGACCTTGGCCCAACCAATGGCCCGAGAGCAATTACCTTCATCTCTGGCTCTGCT 195
DB 119 GACCCCAAGGACCTTGGCCCAACCAATGGCCCGAGAGCAATTACCTTCATCTCTGGCTCTGCT 178
QY 196 GAGCGGCGCTTGGTTCCTCCACCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 255
DB 179 GAGCGGCGCTTGGTTCCTCCACCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 238
QY 256 TGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 315
DB 239 TGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 298
QY 316 GTGCGGGGATGCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 375
DB 299 GTGCGGGGATGCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 358
QY 376 AACTGGGCCAAGGAGCAATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 435
DB 359 AACTGGGCCAAGGAGCAATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418
QY 436 CGGGATGGCCAGCGGCTCAGTCAACCATGGGAGAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
DB 419 CGGGATGGCCAGCGGCTCAGTCAACCATGGGAGAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478
QY 496 CTCA 499
DB 479 CTCA 482
RESULT 14
AW589267/c 370 bp mRNA linear EST 22-MAR-2000
LOCUS xB27907.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2770908 3',
DEFINITION mRNA sequence.
ACCESSION AW589267
VERSION AW589267.1 GI:7276374
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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```
REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 361.
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1. 370
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adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ut2"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
ORIGIN
Query Match 21.6%; Score 370; DB 1; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-178;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1327 GGCTGACTGGGTTCTCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATCTCCTTG 1386
DB 370 GGCTGACTGGGTTCTCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATCTCCTTG 311
QY 1387 CATCCCGAGCTGTGTGATCCCTGCCAGGCCCCCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1446
DB 310 CATCCCGAGCTGTGTGATCCCTGCCAGGCCCCCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
QY 1447 GGCTGATCATGGAAGTAAAGGAGTTAGGCAATTCATCTCTGGGAGTGAAACCTGACTCCA 1506
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QY 1507 TCCCCCTATTGCCACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAATTCACA 1566
DB 190 TCCCCCTATTGCCACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAATTCACA 131
QY 1567 GTTAAAGAGCTTATCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1626
DB 130 GTTAAAGAGCTTATCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 71
QY 1627 TATGTTAAGGAGTGTGTTCTTGGCTGATGTTCTGCTATCTTAACTTAACTGACACAGT 1686
DB 70 TATGTTAAGGAGTGTGTTCTTGGCTGATGTTCTGCTATCTTAACTTAACTGACACAGT 11
QY 1687 TTGTAAGTAC 1696
DB 10 TTGTAAGTAC 1
RESULT 15
CD702656 513 bp mRNA linear EST 25-JUN-2003
LOCUS EST19181 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION CD702656
ACCESSION CD702656
VERSION CD702656.1 GI:32233286
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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 513)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsmu.edu.cn.
FEATURES
source
1..513
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Query Match 18.9%; Score 323; DB 6; Length 513;
Best Local Similarity 100.0%; Pred. No. 3e-154;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1115 GGTACCCAGAACCATGATCATCTTCCAGGGCACCCAGACAGACTCGTGGGGGCAC 1174
DB 74 GGTACCCAGAACCATGATCATCTTCCAGGGCACCCAGACAGACTCGTGGGGGCAC 113
QY 1175 CTTGTCTCAGGTGTACTGTAACCCCTGCAGGCCAGTGCACACCCCTTCTGGGAG 1234
DB 134 CTTGTCTCAGGTGTACTGTAACCCCTGCAGGCCAGTGCACACCCCTTCTGGGAG 193
QY 1235 AAGCATGGCTACAGAAATCAAGAGGGGGACAGAAACCCCTGTGGGAGAGGCTTAGACCT 1294
DB 194 AAGCATGGCTACAGAAATCAAGAGGGGGACAGAAACCCCTGTGGGAGGCTTAGACCT 253
QY 1295 GAAGCATGCCCCACTCTGGCTCCTCTGCTTGGCTGACTGGGTTCTTGACCATGTGCA 1354
DB 254 GAAGCATGCCCCACTCTGGCTCCTCTGCTTGGCTGACTGGGTTCTTGACCATGTGCA 313
QY 1355 TTTCAGTGGCCATGGGATACATCTCTTGCATCCCGAGCTGGTCTGATCCCTGCCAG 1414
DB 314 TTTCAGTGGCCATGGGATACATCTCTTGCATCCCGAGCTGGTCTGATCCCTGCCAG 373
QY 1415 GGCCCTCTCTCTCTCTCTCATGG 1437
DB 374 GGCCCTCTCTCTCTCTCATGG 396
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AI702452/c 330 bp mRNA linear EST 16-DEC-1999
LOCUS tz94b12.x1 NCI_CGAP_Kid11 Homo sapiens cdna clone IMAGE:2296223 3',
DEFINITION mRNA sequence.
ACCESSION AI702452
VERSION AI702452.1 GI:4990352
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 330)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 236 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..330
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2296223"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 18.7%; Score 321; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 3.1e-153;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1376 ACATCTCTTGCATCCCGAGTGTGATCCCTGCCAGGGCCCTTCTCTCTGCTCAT 1435
DB 330 ACATCTCTTGCATCCCGAGTGTGATCCCTGCCAGGGCCCTTCTCTCTGCTCAT 271
QY 1436 GGTCTTCAGTGGCTGATCATGGAAGTAAGAGTTAGGCATTACCTTCTGGAGTGAA 1495
DB 270 GGTCTTCAGTGGCTGATCATGGAAGTAAGAGTTAGGCATTACCTTCTGGAGTGAA 211
QY 1496 CCTGACTCATCCCGCTATTGCCACCTTAACCAATCATGCCAACTTCTCCCTCCCTGG 1555
DB 210 CCTGACTCATCCCGCTATTGCCACCTTAACCAATCATGCCAACTTCTCCCTCCCTGG 151
QY 1556 GTAATTCAACAGTTAAAGAGCTTATCTTAATGTATTGTATGGGGGGTGGCGAGGC 1615
DB 150 GTAATTCAACAGTTAAAGAGCTTATCTTAATGTATTGTATGGGGGGTGGCGAGGC 91
QY 1616 CCACCTATGTATTGTAAAGAGTGTGGTCTGGTCTCTGGCTGATGTTCTGTATCTTAAC 1675
DB 90 CCACCTATGTATTGTAAAGAGTGTGGTCTGGTCTCTGGCTGATGTTCTGTATCTTAAC 31
QY 1676 ATGACCACAGTTTGTAAAGTAC 1696
DB 30 ATGACCACAGTTTGTAAAGTAC 10
RESULT 17
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LOCUS BE741035
DEFINITION 601594018F1 NIH_MGC_9 Homo sapiens cdna clone IMAGE:3947861 5',
ACCESSION BE741035
VERSION BE741035.1 GI:10155027
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1015)
NTH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMB10 row: d column: 06
High quality sequence stop: 752.
Location/Qualifiers
1. .1015
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/notes="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
Query Match 17.7%; Score 303; DB 2; Length 1015;
Best Local Similarity 99.5%; Pred. No. 6.4e-144;
Matches 403; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 204 CCTTGAGTCCCCACCTGCTGCTGCGGACCTGCGGAGCTGTCGCGGG 263
DB 147 CCTTGAGTCCCCACCTGCTGCTGCGGACCTGCGGAGCTGTCGCGGG 206
QY 264 TGCTTCTGCTTCCGCGCTGCGGAGTTCCTCCAGCGCTGTGAGCCTGTGCGGG 323
DB 207 TGCTTCTGCTTCCGCGCTGCGGAGTTCCTCCAGCGCTGTGAGCCTGTGCGGG 266
QY 324 ATGACGCCCCCTGCTGTCTACTGAGGACTCCATGAGGGGACTGCTGAAAGCCAACTGGGC 383
DB 267 ATGACGCCCCCTGCTGTCTACTGAGGACTCCATGAGGGGACTGCTGAAAGCCAACTGGGC 326
QY 384 CAAAGGAGCAATGGAGTGGCCCGGAGCTGCTGACCTGATGTCACCCCGCGGGGATGG 443
DB 327 CAAAGGAGCAATGGAGTGGCCCGGAGCTGCTGACCTGATGTCACCCCGCGGGGATGG 386
QY 444 CCAGCGGCTCAAGTCAACATGGGAGCAGCTTCAGCTACCCCGGAGTGTAAAGCTCAAAGG 503
DB 387 CCAGCGGCTCAAGTCAACATGGGAGCAGCTTCAGCTACCCCGGAGTGTAAAGCTCAAAGG 446
QY 504 CATCCCTGTGTATCCCTTACCCGAGGGCCACTCCCGAGGCCCTGTATGCGGACTCTCTGCTG 563
DB 447 CATCCCTGTGTATCCCTTACCCGAGGGCCACTCCCGAGGCCCTGTATGCGGACTCTCTGCTG 506
QY 564 CAAAGGAGCAACTGGCGATCCCGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 608
DB 507 CAAAGGAGCAACTGGCGGATCCCGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 551

RESULT 18
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LOCUS
AA573775 556 bp mRNA linear EST 12-SEP-1997

DEFINITION nk07d10.s1 NCI_CGAP_Co2 Homo sapiens cDNA clone IMAGE:1012819 3',
mRNA sequence.
AA573775
VERSION AA573775.1 GI:2348290
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 556)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 635 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 465.
Location/Qualifiers
1. .556
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/clone_lib="NCI_CGAP_Co2"
/notes="Organ: Colon; Vector: Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Bulk colon villous adenoma. 5' adaptor sequence:
5' GAATTCGGCAGCG 3' 3' adaptor sequence: 5'
CTCAGATTTTTTTTTTTTTTTT 3' Average insert size: 1.1 kb."
ORIGIN
Query Match 17.0%; Score 291; DB 1; Length 556;
Best Local Similarity 99.6%; Pred. No. 9.1e-138;
Matches 461; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1141 TTCCAGGGCACCGACACAGACTCGTCGGGGGACCCCTTGTCTCAGGTGTACTGTACCC 1200
DB 556 TTCCAGGGCACCGACACAGACTCGTCGGGGGACCCCTTGTCTCAGGTGTACTGTACCC 497
QY 1201 CTGCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGGCTACAGATGAGAGGG 1260
DB 496 CTGCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGGCTACAGATGAGAGGG 437
QY 1261 GGACACAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCTCCTCTCTCC 1320
DB 436 GGACACAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCTCCTCTCTCC 377
QY 1321 TGCCTTGGCTGACTGGGTTCTTGACCATGTGCAATTTC-ACTGGGCCATGGGATCTACAT 1379
DB 376 TGCCTTGGCTGACTGGGTTCTTGACCATGTGCAATTTC-ACTGGGCCATGGGATCTACAT 317
QY 1380 CTCCTTGCATCCCGAGCTGTGATCCCTGCCAGGGCCCTTCTCTCTCTCATGGTC 1439
DB 316 CTCCTTGCATCCCGAGCTGTGATCCCTGCCAGGGCCCTTCTCTCTCTCATGGTC 257
QY 1440 TTCAGGTGGCTGATCATGAAAGTAAAGAGTTTACCATTTACCTTCTGGGAGTGAACCT 1499
DB 256 TTCAGGTGGCTGATCATGAAAGTAAAGAGTTTACCATTTACCTTCTGGGAGTGAACCT 197

QY 1500 GACTCCATCCCTATTGCGACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAA 1559
|||||
Db 196 GACTCCATCCCTATTGCGACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAA 137
|||||
QY 1560 TTCAACAGTTAAAGAAGCTTATCTTAAATGATTTGTTATGGG 1602
|||||
Db 136 TTCAACAGTTAAAGAAGCTTATCTTAAATGATTTGTTATGGG 94
|||||

RESULT 19
A1216202/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
1. .412
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1884036"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu5"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 14.2%; Score 244; DB 1; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.4e-113;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1438 TCTTCAGGTGGCTGATCATGGAAGTAGGAGTTAGGCATTACCTTCTGGGAGTGAACC 1497
|||||
Db 274 TCTTCAGGTGGCTGATCATGGAAGTAGGAGTTAGGCATTACCTTCTGGGAGTGAACC 215
|||||
QY 1498 CTGACTCCATCCCTATTGCGACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGT 1557
|||||
Db 214 CTGACTCCATCCCTATTGCGACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGT 155
|||||
QY 1558 AATTCAACAGTTAAAGAAGCTTATCTTAAATGATTTGTTATGGGGGTGGGAGGGCCC 1617
|||||
Db 154 AATTCAACAGTTAAAGAAGCTTATCTTAAATGATTTGTTATGGGGGTGGGAGGGCCC 95
|||||

QY 1618 ACTCTATGTTATGTTAAGGAGTTGGTTCTGGTCTTGGCTGATGTTCTCTATCTTAACAT 1677
|||||
Db 94 ACTCTATGTTATGTTAAGGAGTTGGTTCTGGTCTTGGCTGATGTTCTCTATCTTAACAT 35
|||||
QY 1678 GACC 1681
|||||
Db 34 GACC 31
|||||

RESULT 20
AW008047/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
1. .423
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2532827"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH10B"
/clone_lib="NCI CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

Query Match 12.6%; Score 215; DB 1; Length 423;
Best Local Similarity 99.5%; Pred. No. 1.2e-98;
Matches 385; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1311 TGGCTCTCTCTGCTTGGCTGACTGGGTTCTCGGACCATGTGCATTCTACTGGGCATGG 1370
Db 393 TGGCTCTCTCTGCTTGGCTGACTGGGTTCTCGGACCATGTGCATTCTACTGGGCATGG 334
|||||
QY 1371 GATCTACATCTCTTGGCATCCCATCCCGAGTGTGTGATCCCTGCCAGGGCCCTTCTCTCTG 1430
Db 333 GATCTACATCTCTTGGCATCCCATCCCGAGTGTGTGATCCCTGCCAGGGCCCTTCTCTCTG 274
|||||
QY 1431 CTCATGGTCTTCAGGTGGCTCATCATGGAAGTAGGAGTTAGGCATTACCTTCTGGGA 1490
Db 273 CTCATGGTCTTCAGGTGGCTCATCATGGAAGTAGGAGTTAGGCATTACCTTCTGGGA 214
|||||

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QY 1491 GTGAACCTGACTCC-ATCCCCCTATTGGCCACCTTAACCAATCATGCAAACTTCTCCCTC 1549
Db 213 GTGAACCTGACTCCAAATCCCTTATTGGCCACCTTAACCAATCATGCAAACTTCTCCCTC 154
QY 1550 CCTGGGGTAATTCAACAGTTAAAGAGAGCTTATCTTAAATGTTATTGTTATGGGGGGTGGG 1609
Db 153 CCTGGGGTAATTCAACAGTTAAAGAGAGCTTATCTTAAATGTTATTGTTATGGGGGGTGGG 94
QY 1610 CAGGGCCCACTCTATGTTATTGTTAAAGAGAGTGGTCTGGTCTTGGCTGAGTGTCTGTAT 1669
Db 93 CAGGGCCCACTCTATGTTATTGTTAAAGAGAGTGGTCTGGTCTTGGCTGAGTGTCTGTAT 34
QY 1670 CTTAACAATGACCAAGTTTCTAGTAC 1696
Db 33 CTTAACAATGACCAAGTTTCTAGTAC 7
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RESULT 21
BE162756
LOCUS BE162756 244 bp mRNA linear EST 21-JUN-2000
DEFINITION PM1-HT0454-170100-003-f07 HT0454 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE162756
VERSION BE162756.1 GI:8625477
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 244)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM1-HT0454-170
100-003-f07&t3=2000-01-17&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 244.
```

```
FEATURES
source
1. 244
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0454"
/notes="Organ: head neck; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters patent application
No. 196, 716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
```

ORIGIN

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Query Match 12.4%; Score 213; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.2e-97;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 267 CTTCTGTTCCGCGCTGCGGGATTGCTTCAGCGCTGTGAGCCTGTGTGCGGGGATG 326
Db 29 CTTCTGTTCCGCGCTGCGGGATTGCTTCAGCGCTGTGAGCCTGTGTGCGGGGATG 88
QY 327 CAGCCCCCTGCTGTCTACTGAGGACTCCACTGAGGGGACTGCTGAAGCCAACTGGGCCAA 386
Db 89 CAGCCCCCTGCTGTCTACTGAGGACTCCACTGAGGGGACTGCTGAAGCCAACTGGGCCAA 148
QY 387 GGAGCACAATGGAGTGGCCCCCAGCCCTGATCGTGCACCCCGGCGGGGATGGCCA 446
Db 149 GGAGCACAATGGAGTGGCCCCCAGCCCTGATCGTGCACCCCGGCGGGGATGGCCA 208
QY 447 GCGGCTCAAGTCAACCATGGGCGAGCAGCTTCAG 479
Db 209 GCGGCTCAAGTCAACCATGGGCGAGCAGCTTCAG 241
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RESULT 22
BM750392
LOCUS BM750392 246 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0025949 S7SNU719 Homo sapiens cDNA clone S7SNU719-1-G12 5',
mRNA sequence.
ACCESSION BM750392
VERSION BM750392.1 GI:19080010
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 246)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 1 row: G column: 12
High quality sequence stop: 246.
```

```
FEATURES
source
1. 246
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S7SNU719-1-G12"
/sex="M"
/tissue_type="Stomach"
/cell_type="Epithelial"
/cell_line="SNU-719"
/lab_host="Top10F"
/clone_lib="S7SNU719"
/notes="Organ: Stomach; Vector: pcNS; Site:1: EcoRI;
Site:2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transfection of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
```

full-length enriched cDNA library."

ORIGIN

Query Match 12.1%; Score 208; DB 3; Length 246;
Best Local Similarity 100.0%; Pred. No. 4.7e-95;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1489 GAGTGAACCTGACTCCATCCCTATTCGCCACCTTAACCAATCATGCAAACTTCCTCCCT 1548
|||||
DB 28 GAGTGAACCTGACTCCATCCCTATTCGCCACCTTAACCAATCATGCAAACTTCCTCCCT 87
|||||

QY 1549 CCCTGGGGTAATTCACACAGTTAAAGAAAGCTTATCTTAAATGATTTATTTGGGGGGTGG 1608
|||||

DB 88 CCCTGGGGTAATTCACACAGTTAAAGAAAGCTTATCTTAAATGATTTATTTGGGGGGTGG 147
|||||

QY 1609 GCAGGGCCCACTATGTTATGTTAAGGAGTTGGTCTGGTCTGGCTGATGTTCTGTA 1668
|||||

DB 148 GCAGGGCCCACTATGTTATGTTAAGGAGTTGGTCTGGTCTGGCTGATGTTCTGTA 207
|||||

QY 1669 TCTTACATGACCACAGTTTGTAAAGTAC 1696
|||||

DB 208 TCTTACATGACCACAGTTTGTAAAGTAC 235
|||||

RESULT 23

BG998476

LOCUS BG998476 291 bp mRNA linear EST 13-JUN-2001

DEFINITION MR4-HT1265-170401-002-d07 HT1265 Homo sapiens cDNA, mRNA sequence.

ACCESSION BG998476

VERSION BG998476.1 GI:14402546

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 291)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-HT1265-170401-002-d07&t3=2001-04-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 284.

FEATURES

source

1. .291
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT1265"
/note="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 10.5%; Score 180; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.3e-80;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1517 GCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAATTCACACAGTTAAAGAA 1576
|||||

DB 60 GCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAATTCACACAGTTAAAGAA 119
|||||

QY 1577 GCTTATCTTAAATGATTTATTTGGGGGTGGGAGGCCCACTCTATGTTATGTTAAGG 1636
|||||

DB 120 GCTTATCTTAAATGATTTATTTGGGGGTGGGAGGCCCACTCTATGTTATGTTAAGG 179
|||||

QY 1637 AGTTGGTCTGGTCTTCTTGGCTGATGTTCTGATCTTAAACATGACCACAGTTTGTAAAGTAC 1696
|||||

DB 180 AGTTGGTCTGGTCTTCTTGGCTGATGTTCTGATCTTAAACATGACCACAGTTTGTAAAGTAC 239
|||||

RESULT 24

BE409561

LOCUS BE409561 1092 bp mRNA linear EST 21-JUL-2000

DEFINITION 601299865F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629848 5', mRNA sequence.

ACCESSION BE409561

VERSION BE409561.1 GI:9346011

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1092)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM317 row: a column: 17
High quality sequence start: 19
High quality sequence stop: 482.

FEATURES

source

1. .1092
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3629848"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 9.1%; Score 156; DB 2; Length 1092;
Best Local Similarity 100.0%; Pred. No. 3.3e-68;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY 54 GTGGAGCGCCACAGAGCTATGCTCTGGAGACATATGATTAACCACTCAGCCGCCACC 113
Db 158 GTGGAGCGCCACAGAGCTATGCTCTGGAGACATATGATTAACCACTCAGCCGCCACC 217
QY 114 AAGCGCGCCGACCCGTAGACACAGACCCCAAGAGCCCTGGCCACCACCATGGCCAGAGAGCAT 173
Db 218 AAGCGCGCCGACCCGTAGACACAGACCCCAAGAGCCCTGGCCACCACCATGGCCAGAGAGCAT 277
QY 174 TACCTTCATCTCTGGCTCTGCTGAGCGCGCCCTTGA 209
Db 278 TACCTTCATCTCTGGCTCTGCTGAGCGCGCCCTTGA 313

RESULT 25
BE741110 623 bp mRNA linear EST 15-SEP-2000
LOCUS 601593919F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947885 5',
DEFINITION mRNA sequence.
ACCESSION BE741110
VERSION BE741110.1 GI:10155102
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 623)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.lln.gov
Plate: L1CM810 row: e column: 06
High quality sequence stop: 615.
FEATURES
    source
    1..623
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:3947885"
        /tissue_type="adenocarcinoma cell line"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH_MGC_9"
        /notes="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
        EcoRI; cDNA made by oligo-dT priming. Directionally
        cloned into EcoRI/XhoI sites using the following 5',
        adaptor: GGCAAGGACCTGGCCACCATGGCCAGAGAGCATTAACCTTCATCTCTGGCTCTGCT 195
        insert size 1.8kb. Library constructed by Ling Hong in
        the laboratory of Gerald M. Rubin (University of
        California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

```
Query Match 8.5%; Score 145; DB 2; Length 623;
Best Local Similarity 100.0%; Pred. No. 1.4e-62;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GACCCCAAGGACCTTGGCCACCATGGCCAGAGAGCATTAACCTTCATCTCTGGCTCTGCT 195
Db 85 GACCCCAAGGACCTTGGCCACCATGGCCAGAGAGCATTAACCTTCATCTCTGGCTCTGCT 144

QY 196 GAGCGCGCCCTTGAAGTCCCCACACCTGCTGCTCTGGCGACCCCTGGGTGTGGAGTGG 255
Db 145 GAGCGCGCCCTTGAAGTCCCCACACCTGCTGCTCTGGCGACCCCTGGGTGTGGAGTGG 204

QY 256 TGCGGGGCTCCTTCTGCTTCGGCC 280
|||||
```

Db 205 TGCGGGGCTCCTTCTGCTTCGGCC 229

RESULT 26

```
AW732798 139 bp mRNA linear EST 21-APR-2000
LOCUS bb14f07.y1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2962885 5',
DEFINITION mRNA sequence.
ACCESSION AW732798
VERSION AW732798.1 GI:7633136
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 139)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.lln.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 112.
FEATURES
    source
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:2962885"
        /tissue_type="choriocarcinoma"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH_MGC_21"
        /notes="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
        Site 2: EcoRI; cDNA made by oligo-dT priming.
        Directionally cloned into EcoRI/XhoI sites using the
        following 5' adaptor: GGCAAGGAC(G). Size-selected >500bp
        for average insert size 1.8kb. Library constructed by
        Ling Hong in the laboratory of Gerald M. Rubin (University
        of California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

```
Query Match 8.1%; Score 139; DB 1; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 378 CTGGGCCAAGGACCAATGGAGTGGCCCCCAGCCCTGATCGTGACCCCGCCGCGGCG 437
Db 1 CTGGGCCAAGGACCAATGGAGTGGCCCCCAGCCCTGATCGTGACCCCGCCGCGGCG 60

QY 438 GGATGGCCAGCGGCTCAAGTCAACCATGGCAGCAGCTTCAGCTACCCCGATGTTAAGCT 497
Db 61 GGATGGCCAGCGGCTCAAGTCAACCATGGCAGCAGCTTCAGCTACCCCGATGTTAAGCT 120

QY 498 CAAAGGCATCCCTGTGTAT 516
Db 121 CAAAGGCATCCCTGTGTAT 139

RESULT 27
BF856421 450 bp mRNA linear EST 16-JAN-2001
LOCUS RC0-FN0204-221200-022-b01 FN0204 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BF856421
VERSION BF856421.1 GI:12244165
```

KEYWORDS	EST.	Homo sapiens (human)	Homo sapiens (human)	
SOURCE	Homo sapiens	Homo sapiens	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 450)	1 (bases 1 to 277)	1 (bases 1 to 277)	
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jorgensen,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.	
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	21C Frontier Korean EST Project 2001	21C Frontier Korean EST Project 2001	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	Unpublished (2002)	Unpublished (2002)	
PUBMED	10737800	Contact: Kim YS	Contact: Kim YS	
COMMENT	Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC0&t2=RC0-FN0204-221200-022-b01&t3=2000-12-22&t4=1) Seq primer: puc 18 forward High quality sequence start: 72 High quality sequence stop: 446.	Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 20 row: C column: 05 High quality sequence stop: 277.	Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 20 row: C column: 05 High quality sequence stop: 277.	
FEATURES	source 1..450 Location/Qualifiers /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="FN0204" /note="Organ: prostate normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No.196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."	source 1..277 Location/Qualifiers /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="S9SNU601-20-C05" /sex="M" /tissue_type="Ascites" /cell_type="Epithelial" /cell_line="SNU-601" /lab_host="Top10F" /clone_lib="S9SNU601" /note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI; Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18S-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	source 1..277 Location/Qualifiers /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="S9SNU601-20-C05" /sex="M" /tissue_type="Ascites" /cell_type="Epithelial" /cell_line="SNU-601" /lab_host="Top10F" /clone_lib="S9SNU601" /note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI; Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18S-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	source 1..277 Location/Qualifiers /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="S9SNU601-20-C05" /sex="M" /tissue_type="Ascites" /cell_type="Epithelial" /cell_line="SNU-601" /lab_host="Top10F" /clone_lib="S9SNU601" /note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI; Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18S-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
ORIGIN	Query Match 6.4%; Score 109; DB 2; Length 450; Best Local Similarity 99.4%; Pred. No. 4.9e-44; Matches 159; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Query Match 5.9%; Score 101; DB 3; Length 277; Best Local Similarity 100.0%; Pred. No. 6.1e-40; Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match 5.9%; Score 101; DB 3; Length 277; Best Local Similarity 100.0%; Pred. No. 6.1e-40; Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match 5.9%; Score 101; DB 3; Length 277; Best Local Similarity 100.0%; Pred. No. 6.1e-40; Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1420 CTTCTCTCTGCTCATGGTCTTCAGGTGGCGCTGATCATGAAAGTAAAGGTTAGGCATT 1479	35 GGCCTCCACGCTTGGGACCGTGGAGCGGCCAACAGAGTATGCTCTGGAGACATATGATA 94	35 GGCCTCCACGCTTGGGACCGTGGAGCGGCCAACAGAGTATGCTCTGGAGACATATGATA 94	35 GGCCTCCACGCTTGGGACCGTGGAGCGGCCAACAGAGTATGCTCTGGAGACATATGATA 94
Db	196 CTTCTCTCTGCTCATGGTCTTCAGGTGGCGCTGATCATGAAAGTAAAGGTTAGGCATT 255	86 GGCCTCCACGCTTGGGACCGTGGAGCGGCCAACAGAGTATGCTCTGGAGACATATGATA 145	86 GGCCTCCACGCTTGGGACCGTGGAGCGGCCAACAGAGTATGCTCTGGAGACATATGATA 145	86 GGCCTCCACGCTTGGGACCGTGGAGCGGCCAACAGAGTATGCTCTGGAGACATATGATA 145
QY	1480 ACCTTCGGAGTGAACCTTGATCCATCCCTTATGACCCCTAACCAATCATGCAAA 1539	95 AACCACTCAGCCCCCACCAGCCGCGCCGACCGTAGACCA 135	95 AACCACTCAGCCCCCACCAGCCGCGCCGACCGTAGACCA 135	95 AACCACTCAGCCCCCACCAGCCGCGCCGACCGTAGACCA 135
Db	256 ACCTTCGGAGTGAACCTTGATCCATCCCTTATGACCCCTAACCAATCATGCAAA 315	146 AACCACTCAGCCCCCACCAGCCGCGCCGACCGTAGACCA 186	146 AACCACTCAGCCCCCACCAGCCGCGCCGACCGTAGACCA 186	146 AACCACTCAGCCCCCACCAGCCGCGCCGACCGTAGACCA 186
QY	1540 CTTCTCCCTCCCTGGGGTAAATCAACAGTTTAAAGAAGCT 1579			
Db	316 CTTCTCCCTCCCTGGGGTAAATCAACAGTTTAAAGAAGCT 355			
RESULT 28	BO081980	CR763815	CR763815	CR763815
LOCUS	K-EST0026481 S9SNU601 Homo sapiens cDNA clone S9SNU601-20-C05 5', mRNA sequence.	276 bp mRNA linear EST 23-SEP-2004	276 bp mRNA linear EST 23-SEP-2004	276 bp mRNA linear EST 23-SEP-2004
DEFINITION		DKFZp469G0138 r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone DKFZp469G0138 5', mRNA sequence.	DKFZp469G0138 r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone DKFZp469G0138 5', mRNA sequence.	DKFZp469G0138 r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone DKFZp469G0138 5', mRNA sequence.
ACCESSION	BO081980	CR763815	CR763815	CR763815
VERSION	BQ081980	EST.	EST.	EST.
KEYWORDS	BQ081980.1 GI:19938986	Pongo pygmaeus (orangutan)	Pongo pygmaeus (orangutan)	Pongo pygmaeus (orangutan)
	EST.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 276)
Ansoerge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
Wewes,H.W., Weil,B., Amid,C., Oeanger,A., Fobo,G., Han,M. and
Wiemann,S.
Pongo pygmaeus mRNA (Ansoerge,W., Krieger,S., Regiert,T., et al.)
Unpublished (2004)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; riin, Germany. Please contact
RZPD for ordering.
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469G0138
Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.

FEATURES
source
Location/Qualifiers
1..276
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469G0138"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN
Query Match 5.7%; Score 97; DB 7; Length 276;
Best Local Similarity 99.3%; Pred. No. 7e-38;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAGCGCCACAGAGCTATGCTGGAGACATATGATAAACCTCAGCCGCCACCAAGC 117
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Db 120 GAGCGCCACAGAGCTATGCTGGAGACATATGATAAACCTCAGCCGCCACCAAGC 179
|||||
QY 118 CGCGGACCCGTAGACAGACCCAGGACCCCTGGCCACCATGGGCGAGAGCATTACC 177
|||||
Db 180 CGCGGACCCGTAGACAGACCCAGGACCCCTGGCCACCATGGGCGAGAGCATTACC 239
|||||
QY 178 TTCACTCTGGCTCTGCTGAGCGGCC 205
|||||
Db 240 TTCACTCTGGCTCTGCTGAGCGGCC 267
|||||

RESULT 30
BG335647
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

602404274F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4541898 5',
mRNA sequence.
BG335647
BG335647.1 GI:13142085
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 928)
NIH-MGC <http://img.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA library preparation: Ling Hong/Rubin Laboratory
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 928)
Ansoerge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
Wewes,H.W., Weil,B., Amid,C., Oeanger,A., Fobo,G., Han,M. and
Wiemann,S.
Pongo pygmaeus mRNA (Ansoerge,W., Krieger,S., Regiert,T., et al.)
Unpublished (2004)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; riin, Germany. Please contact
RZPD for ordering.
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469G0138
Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.

FEATURES
source
Location/Qualifiers
1..928
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4541898"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 21"
/note="Organ: Placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 5.7%; Score 97; DB 2; Length 928;
Best Local Similarity 100.0%; Pred. No. 7.9e-38;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCCCGCCCTGGACACCCCGCCCGCCAGCATCTGGCCCTCCACGCTTGGACCGTGGAG 60
|||||
Db 103 ATGCCCCCGCCCTGGACACCCCGCCCGCCAGCATCTGGCCCTCCACGCTTGGACCGTGGAG 162
|||||
QY 61 CGGCCACAGAGCTATGCTGGAGACATATGATAAAC 97
|||||
Db 163 CGGCCACAGAGCTATGCTGGAGACATATGATAAAC 199
|||||

RESULT 31
AG071655
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AG071655
Pan troglodytes DNA, clone: PTB-062016.F, genomic survey sequence.
AG071655
AG071655.1 GI:16623457
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
1
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 677)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
E-mail: chimpsgsc.riken.go.jp, URL:<http://hgp.gsc.riken.go.jp/>,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1..677
/organism="Pan troglodytes"

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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-062016.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          5.0%; Score 86; DB 10; Length 677;
Best Local Similarity 100.0%; Pred.No. 3.6e-32; Indels 0; Gaps 0;
Matches 86; Conservative 0; Mismatches 0;

QY 1244 CTACAGATGAAGAGGGGACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTG 1303
Db 301 CTACAGATGAAGAGGGGACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTG 360

QY 1304 CCACCTCTGGCTCCTCTCCTCGCTTGGC 1329
Db 361 CCACCTCTGGCTCCTCTCCTCGCTTGGC 386

RESULT 32
BF191474
LOCUS          537 bp mRNA linear EST 02-NOV-2000
DEFINITION    239074 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION    BF191474
VERSION      BF191474.1 GI:11074843
KEYWORDS     EST.
SOURCE       Sus scrofa (pig)
ORGANISM     Sus scrofa
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
              Sus.
REFERENCE     1 (bases 1 to 537)
AUTHORS      Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
              Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
              Quackenbush,J. and Keele,J.W.
              Porcine gene discovery by normalized cDNA-library sequencing and
              EST cluster assembly
              Mamm. Genome 13 (8), 475-478 (2002)
              12226715
              Contact: Smith TPL
              USDA, ARS, US Meat Animal Research Center
              PO Box 166, Clay Center, NE 68933-0166, USA
              Tel: 402 762 4366
              Fax: 402 762 4390
              Email: smith@email.marc.usda.gov
              Single pass sequencing. Bases called and alt trimmed with phred
              v0.980904.e. Vector identified by cross_match with the -minscore 18
              and -minmatch 12 options.
              PCR Primers
              FORWARD: AGGAACACGCTATGACCAT
              BACKWARD: GTTTCACGTCACGACG
              Plate: 66 row: F column: 19
              Seq primer: ATTAGTGACACTATAG.
              Location/Qualifiers
              1..537
              /organism="Sus scrofa"
              /mol_type="mRNA"
              /db_xref="taxon:9823"
              /tissue_type="pooled"
              /lab_host="DH10B"
              /clone_lib="MARC 2P1G"
              /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
              Library made from pooled tissue from testis, ovary,
              endometrium, hypothalamus, pituitary, and placenta."

ORIGIN
Query Match          3.4%; Score 59; DB 2; Length 537;
Best Local Similarity 100.0%; Pred.No. 2.8e-18; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 0;

QY 790 TCAGACACTGTGTCTCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCAC 848
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Db 266 TCAGACACTGTGTCTCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCAC 324

RESULT 33
BG335025
LOCUS          1088 bp mRNA linear EST 27-FEB-2001
DEFINITION    602403470F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4541320 5',
              mRNA sequence.
ACCESSION    BG335025
VERSION      BG335025.1 GI:13141463
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
              1 (bases 1 to 1088)
              NIH-MGC http://mgc.nci.nih.gov/.
              National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: c9apbs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM1219 row: k column: 17
              High quality sequence stop: 556.
              Location/Qualifiers
              1..1088
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
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              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH_MGC_21"
              /note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
              Site 2: EcoRI; cDNA made by oligo-dT priming.
              Directionally cloned into EcoRI/XhoI sites using the
              following 5' adaptor: GGCACGAG(G). Size-selected >500bp
              for average insert size 1.8kb. Library constructed by
              Ling Hong in the laboratory of Gerald M. Rubin (University
              of California, Berkeley) using ZAP-cDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies).".

ORIGIN
Query Match          3.4%; Score 58; DB 2; Length 1088;
Best Local Similarity 100.0%; Pred.No. 9.9e-18; Indels 0; Gaps 0;
Matches 58; Conservative 0; Mismatches 0;

QY 154 CACCATGGGCCAGAGAGCATTTACCTTCATCTCTGGCTCTGCTGAGCGCCCTTGAGT 211
Db 285 CACCATGGGCCAGAGAGCATTTACCTTCATCTCTGGCTCTGCTGAGCGCCCTTGAGT 342

RESULT 34
AW435934
LOCUS          321 bp mRNA linear EST 09-JUL-2000
DEFINITION    75034 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION    AW435934
VERSION      AW435934.1 GI:6971177
KEYWORDS     EST.
SOURCE       Sus scrofa (pig)
ORGANISM     Sus scrofa
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
              Sus.
              1 (bases 1 to 321)
```

AUTHORS Fahrenkrug,S.C., Smith,T.P.L., Preking,B.A., Cho,J., White,J., Vallet,J., Wise,I., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush,J. and Keelle,J.W.

TITLE Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly

JOURNAL Mamm. Genome 13 (8), 475-478 (2002)

PUBMED 12226715

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAG
Plate: 30 row: H column: 14
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
source
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="WARC 2PiG"
/note="vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

FEATURES
source
1. .321
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="WARC 2PiG"
/note="vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

ORIGIN
Query Match 2.4%; Score 41; DB 1; Length 321;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 985 GTCGCCCTCAGCTGCCATGAGACCATGGTGGCTCAGG 1025
|||||
55 GTCGCCCTCAGCTGCCATGAGACCATGGTGGCTCAGG 95

Db

RESULT 35
BY707606
LOCUS
DEFINITION BY707606 RIKEN full-length enriched, 10 day old male pancreas Mus EST. 16-DEC-2002
musculus cDNA clone 1810019J16 5', mRNA sequence.

ACCESSION BY707606
VERSION BY707606.1 GI:27118783
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus;

REFERENCE
1 (bases 1 to 1009)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schombach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Sult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawai,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,N., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN Integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
Location/Qualifiers
1. .1009
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1810019J16"
/sex="male"
/tissue_type="pancreas"
/dev_stage="10 day old"
/clone_lib="RIKEN full-length enriched, 10 day old male pancreas"

ORIGIN
Query Match 2.3%; Score 39; DB 5; Length 1009;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 835 ATCAGCAGCATCAGCAGGACTACCATCGATGAGCAG 873
|||||
Db 879 ATCAGCAGCATCAGCAGGACTACCATCGATGAGCAG 917
|||||

RESULT 36

Sciuognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 491)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:665694
 Seq primer: -28ml3 rev2 ET from Amersham.

FEATURES
 source
 Location/Qualifiers
 1..491
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:1263142"
 /sex="male"
 /tissue_type="Thymus"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /clone_lib="Soares thymus 2NDMT"
 /notes="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGGAGCGCGGATTTTGTGTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 2.2%; Score 38; DB 1; Length 491;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGAGTACCACCTGGATGACCA 872
 |||||
 Db 74 ATCAGCAGCATCAGCAGGAGTACCACCTGGATGACCA 111
 |||||

RESULT 39
 AI425628
 LOCUS
 DEFINITION
 md57f07.y1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
 clone IMAGE:372517 5', mRNA sequence.

ACCESSION
 AI425628
 VERSION
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 500)
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
 The WashU-NCI Mouse EST Project 1999

TITLE
 The WashU-NCI Mouse EST Project 1999

Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 This read is a RESEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the correct orientation)
 MGI:233949
 Seq primer: -40RP from Gibco
 High quality sequence stop: 468
 POLYA=NO.

FEATURES
 source
 Location/Qualifiers
 1..500
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:372517"
 /sex="unknown"
 /tissue_type="embryo"
 /dev_stage="13.5-14.5dpc total fetus"
 /lab_host="DH10B"
 /clone_lib="Soares mouse embryo NbME13.5 14.5"
 /notes="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGGAGCGCGGAAATTTTGTGTTTTTTTTTTT 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos (total RNA provided by Minoru Ko, Wayne State Univ., from 2); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 2.2%; Score 38; DB 1; Length 500;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGAGTACCACCTGGATGACCA 872
 |||||
 Db 18 ATCAGCAGCATCAGCAGGAGTACCACCTGGATGACCA 55
 |||||

RESULT 40
 AZ059937/c
 LOCUS
 DEFINITION
 RPCI-23-429E10-TV RPCI-23 Mus musculus genomic clone
 RPCI-23-429E10, genomic survey sequence.

ACCESSION
 AZ059937
 VERSION
 AZ059937.1 GI:7351186
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 501)
 Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levine, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html

Plate: 429 row: E column: 10

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

FEATURES

source

1. .501

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-429E10"

/sex="Female"

/lab_host="DH10B"

/clone_lib="RPCI-23"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI MethyIase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 2.2%; Score 38; DB 9; Length 501;

Best Local Similarity 100.0%; Pred. No. 1.8e-07;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGACTACCACTGGATGACCA 872

Db 391 ATCAGCAGCATCAGCAGGACTACCACTGGATGACCA 354

RESULT 41

BE652359

LOCUS

DEFINITION BE652359 519 bp mRNA linear EST 06-SBP-2000

UI-M-A00-aca-d-03-0-UI.r1 NIH_BMAP.MPG Mus musculus cDNA clone

UI-M-A00-aca-d-03-0-UI 5', mRNA sequence.

ACCESSION BE652359

VERSION BE652359.1

KEYWORDS BE652359.1 GI:9978202

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Mus.

1 (bases 1 to 519)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

889548

CONTACT: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mEST@mail.nih.gov

cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements

FEATURES

source

Seq primer: M13 Reverse.

Location/Qualifiers

1. .519

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-A00-aca-d-03-0-UI"

/dev_stage="27-32 days"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NIH BMAP.MPG"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH BMAP.MPG library is a non-normalized library constructed from mouse pineal gland. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Ms. Annie Novakovich, Zivic-Miller Laboratories."

ORIGIN

Query Match 2.2%; Score 38; DB 2; Length 519;

Best Local Similarity 100.0%; Pred. No. 1.8e-07;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGACTACCACTGGATGACCA 872

Db 38 ATCAGCAGCATCAGCAGGACTACCACTGGATGACCA 75

RESULT 42

BQ566109

LOCUS

DEFINITION BQ566109 535 bp mRNA linear EST 19-JUN-2002

Clone gi52a07 5', mRNA sequence.

ACCESSION BQ566109.1

VERSION BQ566109.1

KEYWORDS EST. GI:21469426

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Mus.

1 (bases 1 to 535)

Kachar,B.

EST analysis of gene expression in the mouse Organ of Corti at the

onset of hearing

Unpublished (2002)

Contact: Kachar,B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 52 row: a column: 07

Seq primer: M13RPl reverse primer (ABI).

Location/Qualifiers

1. .535

/organism="Mus musculus"

/mol_type="mRNA"

/strain="BALB/c"

/db_xref="taxon:10090"

/clone="gi52a07"

/sex="male and female"

/dev_stage="Post natal

/clone_lib="Mouse Organ of Corti cDNA pbluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by

cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a Hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25 μ strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

ORIGIN

Query Match 2.2%; Score 38; DB 5; Length 535;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGACTACCACTCGATGAGCA 872

Db 340 ATCAGCAGCATCAGCAGGACTACCACTCGATGAGCA 377

RESULT 43
BG082830

LOCUS BG082830 586 bp mRNA linear EST 18-DEC-2003
DEFINITION H3081C02-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone

ACCESSION BG082830

VERSION BG082830.2 GI:40069253

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 586)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,
Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H.,
Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
10922068

TITLE

JOURNAL

PUBMED

COMMENT

On Jan 26, 2001 this sequence version replaced gi:12565398.
Other ESTs: H3081C02-3
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6920, USA
Email: cdna@lgscn.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit <http://lgscn.grc.nia.nih.gov/cDNA/15k.html> for details.
Plate: H3081 row: C column: 02
Seq primer: -21M13 Reverse
High quality sequence stop: 586
POLYA=No.

FEATURES

source

1..586
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:H3081C02-5"
/db_xref="taxon:10090"
/clone="H3081C02"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA libraries"

/lab_host="DH10B"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A. 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

ORIGIN

Query Match 2.2%; Score 38; DB 2; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGACTACCACTCGATGAGCA 872

Db 99 ATCAGCAGCATCAGCAGGACTACCACTCGATGAGCA 136

RESULT 44

LOCUS BB657667/c

DEFINITION BB657667

musculus cDNA clone D23001M17 5', mRNA sequence.

ACCESSION BB657667

VERSION BB657667.1 GI:16491493

601 bp mRNA linear EST 26-OCT-2001
BB657667 RIKEN full-length enriched, 12 days embryo eyeball Mus


```

Db      462 ATCAGCAGCATCGCAGGACTACCCCTGGATGAGCA 425
|||||
RESULT 46
BI694617
LOCUS   826 bp      mRNA      linear      EST 18-SEP-2001
DEFINITION 603347838F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5375384 5',
mRNA sequence.
ACCESSION BI694617
VERSION   BI694617.1 GI:15657246
KEYWORDS EST.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 826)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1955 row: 1 column: 09
High quality sequence stop: 796.

FEATURES
source
Location/Qualifiers
1..826
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5375384"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 2.2%; Score 38; DB 3; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES
source
Location/Qualifiers
1..826
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5375384"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 2.2%; Score 38; DB 3; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCGCAGGACTACCCCTGGATGAGCA 872
|||||
Db 538 ATCAGCAGCATCGCAGGACTACCCCTGGATGAGCA 575
|||||

RESULT 47
BI694315
LOCUS   918 bp      mRNA      linear      EST 24-OCT-2000
DEFINITION 601787134F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4014680 5',
mRNA sequence.
ACCESSION BI694315
VERSION   BI694315.1 GI:10983355
KEYWORDS EST.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 918)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Donaldo, Ph.D.
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1364 row: k column: 03
High quality sequence start: 28
High quality sequence stop: 840.

FEATURES
source
Location/Qualifiers
1..930
/organism="Mus musculus"
/mol_type="mRNA"

```

```

TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9259 row: d column: 09
High quality sequence stop: 653.

FEATURES
source
Location/Qualifiers
1..918
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:4014680"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu30"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dr. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 2.2%; Score 38; DB 2; Length 918;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCGCAGGACTACCCCTGGATGAGCA 872
|||||
Db 183 ATCAGCAGCATCGCAGGACTACCCCTGGATGAGCA 220
|||||

RESULT 48
BI413848
LOCUS   930 bp      mRNA      linear      EST 14-AUG-2001
DEFINITION 602991514F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5147642 5',
mRNA sequence.
ACCESSION BI413848
VERSION   BI413848.1 GI:15174771
KEYWORDS EST.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 930)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Donaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1364 row: k column: 03
High quality sequence start: 28
High quality sequence stop: 840.

FEATURES
source
Location/Qualifiers
1..930
/organism="Mus musculus"
/mol_type="mRNA"

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/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:5147642"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI CGAP Lu33"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: NotI; Site 2: EcoRI; let
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5',
TGTTCACCAATCTCAAGTGGGAGCGCGCTCTGTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
```

ORIGIN

Query Match 2.2%; Score 38; DB 3; Length 930;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCGAGGACTACCACTGGATGACGA 872
|||||
DB 121 ATCAGCAGCATCAGCGAGGACTACCACTGGATGACGA 158

RESULT 49
BF135747
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF135747 984 bp mRNA linear EST 24-OCT-2000
60178110F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008914 5',
mRNA sequence.
BF135747
BF135747.1 GI:10974696
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 984)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9244 row: d column: 03
High quality sequence stop: 629.

FEATURES
source
1..984
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:4008914"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu30"
/note="Organ: lung; Vector: pCMV-SpORT6; Site 1: NotI;
Site 2: SalI; transgenic model WNT-1, expression driven by
WNTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dr. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 2.2%; Score 38; DB 2; Length 984;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCGAGGACTACCACTGGATGACGA 872
|||||
DB 237 ATCAGCAGCATCAGCGAGGACTACCACTGGATGACGA 274

RESULT 50
AK051860/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK051860 1596 bp mRNA linear HTC 03-APR-2004
Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length
enriched library, clone:D23001M17 product:hypothetical protein,
full insert sequence.
AK051860
AK051860.1 GI:26342255
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

6
(bases 1 to 1596)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
 URL: <http://genome.gsc.riken.jp/>
 URL: <http://fantom.gsc.riken.jp/>.
 Location/Qualifiers
 1. 1596
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 /mol_type="mRNA"
 /strain="C57BL/6J"
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 /db_xref="taxon:10090"
 /clone="D230011M17"
 /tissue_type="eyeball"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="12 days embryo"
 890..1432
 (features="unnamed protein product; hypothetical protein
 [note: decoder, Longest-ORF]
 putative")
 /codon_start=1
 /protein_id="BAC34790.1"
 /db_xref="GI:26342256"
 /translators="MLVLSWPPRRLLGGARSLGGLTPLCSLAQAASADPMGSPADKQ
 GLPRTQAPQRCQSQRKQKXALQSQRRQVGGSLAGSAEPMKVIILGSP
 WPGSLGSLGLVRRPGGWRSSVFSRHNSDGLSQGPKRGPPDDGRGCPGLGMAQMA
 CCSQAPAGRSQEEVRDKLLG"

ORIGIN

Query Match 2.2%; Score 38; DB 4; Length 1596;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGACTACCACCTGGATGACGA 872
 |||||
 DB 519 ATCAGCAGCATCAGCAGGACTACCACCTGGATGACGA 482
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RESULT 51

AK007551
 LOCUS
 DEFINITION
 BINDING PROTEIN (TBP)-ASSOCIATED FACTOR, RNA POLYMERASE II, C1,
 130KD homolog [Mus musculus], full insert sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AK007551 1 GI:12841167
 Mus musculus 10 day old male pancreas cDNA, RIKEN full-length
 enriched library, clone:181001916 product:SIMILAR TO TATA BOX
 BINDING PROTEIN (TBP)-ASSOCIATED FACTOR, RNA POLYMERASE II, C1,
 130KD homolog [Mus musculus], full insert sequence.
 HTG; CAP trapper.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1
 AUTHORS
 TITLE
 JOURNAL
 PUBLISHED
 PAGES

Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 10349636

REFERENCE
 2
 AUTHORS
 TITLE
 JOURNAL
 PUBLISHED
 PAGES

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 11042159

BINDING PROTEIN (TBP)-ASSOCIATED FACTOR, RNA POLYMERASE II, Cl. 130KD homolog [Mus musculus] (SPTR|Q92200, evidence: PASTY, 97.2%ID, 100%length, match=649) putative"

/codon_start=1
/protein_id="BAC25177.1"
/db_xref="GI:26357449"
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ASGAPGVCTGYCLPASDAAGIACSAVGLVCGARAPALSAGDPIEGSAEAAWAKHN
GVPPSPDRAPPRRDQRUKTISMGSSFSYPDVKLGKIPVYPRHATSPVPDVSCKKE
PLAEPPTTHSLPSTPTNSRGSEYYSFHESDLDPENMGSGMSRSEDVLIFFKLT
ELFVHQIDELAKTSDTVFLKTSKISDLISITQDYHLDEQDAEGRLVGRIIRIST
RKRSRSPQSEGRSAPTAAPAPSGHETMLGSLGQDELTVQISQETTADAIARKL
RYPGAPGYPASQSSFGQDTDDSSGAPLLQVVC"

ORIGIN

Query Match 2.2%; Score 38; DB 4; Length 1657;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCCGCGAGCACTACCACTGGATGAGCA 872
|||||
DB 882 ATCAGCAGCATCCGCGAGCACTACCACTGGATGAGCA 919
|||||

RESULT 52

LOCUS AI669760/c 488 bp mRNA linear EST 15-DEC-1999
DEFINITION tui2h08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2250879 3',
mRNA sequence.

ACCESSION AI669760

VERSION AI669760.1 GI:4834534

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 488)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

REFERENCE

AUTHORS

TITLE

Unpublished (1997)

JOURNAL

COMMENT

Email: cgabs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing Arrayed by: Greg Lennon, Ph.D.
Cloning Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 792 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 452.
Location/Qualifiers

FEATURES

source

1. .488
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2250879"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr28"
/notes="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker: plasmid DNA from the
normalized library NCI CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonids

985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 2.2%; Score 37; DB 1; Length 488;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1402 TGATCCCTGCCAGGCCCTTCTTCTCTCATGCT 1438
|||||
DB 352 TGATCCCTGCCAGGCCCTTCTTCTCTCATGCT 316
|||||

RESULT 53

LOCUS BP111348

DEFINITION BP111348 ORCS bovine utero-placenta cDNA Bos taurus CDNA clone
ORCS11684 5', mRNA sequence.

ACCESSION BP111348

VERSION BP111348.1 GI:28313638

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 605)

REFERENCE

AUTHORS

Ishiwata, H., Katsuma, S., Kizaki, K., Patel, O.V., Nakano, H.,
Takahashi, T., Imai, K., Hirasawa, A., Shiojima, S., Ikawa, H.,
Suzuki, Y., Tsujimoto, G., Izaike, Y., Todoroki, J., and Hashizume, K.
Characterization of gene expression profiles in early bovine
pregnancy using a custom cDNA microarray
Mol. Reprod. Dev. 65 (1), 9-18 (2003)
12658628
Contact: Gozoh Tsujimoto
Department of Molecular, Cell Pharmacology
National Research Institute for Child Health and Development
3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan
Tel: 81-3-3149-2476
Fax: 81-3-3149-1252
Email: gtsujimoto@nch.go.jp
This work was performed to collaborate with Developmental Biology
Department, National Institute of Agrobiological Sciences. Address:
2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
81-29-838-8633 e-mail: kazuhao@affrc.go.jp
This work was funded by Organized Research Combination System
(ORCS) project of Ministry of Education, Culture, Sports, Science
and Technology.

FEATURES

source

1. .605
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="ORCS11684"
/tissue_type="mixture of uterus and placenta"
/dev_stage="adult"
/clone_lib="ORCS bovine utero-placenta cDNA"

FEATURES

source

1. .605
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="ORCS11684"
/tissue_type="mixture of uterus and placenta"
/dev_stage="adult"
/clone_lib="ORCS bovine utero-placenta cDNA"

ORIGIN

Query Match 2.0%; Score 35; DB 3; Length 605;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 877 GCTGAGGCGCGCTGTACGCGGCATTCGCAT 911
|||||
DB 57 GCTGAGGCGCGCTGTACGCGGCATTCGCAT 91
|||||

RESULT 54

LOCUS CB463434

DEFINITION CB463434 585 bp mRNA linear EST 26-MAR-2003
723814 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION CB463434


```

VERSION      CB463434.1  GI:29269819
KEYWORDS     EST.
SOURCE       Bos taurus (cow)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
             Pecora; Bovidae; Bovinae; Bos.
REFERENCE    1 (bases 1 to 585)
AUTHORS      Smith,T.P.L., Roberts,A.J., Echterkamp,S.E., Chitko-McKown,C.G.,
             Wray,J.E. and Keefe,J.W.
TITLE        A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL      Unpublished (2003)
COMMENT      Contact: Smith TPL
             USDA, ARS, US Meat Animal Research Center
             PO Box 166, Clay Center, NE 68933-0166, USA
             Tel: 402 762 4366
             Fax: 402 762 4390
             Email: smith@mail.marc.usda.gov
             Single pass sequencing. Bases called with phred v0.020425.c and
             trimmed with the aid of the trim_alt option. Vector identified with
             cross_match v0.990329.
             Plate: LAM8004 row: M column: 8
             Seq primer: GTAATACGACTCACTATAGG.
FEATURES     Location/Qualifiers
             source          1..585
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                        /mol_type="mRNA"
                        /db_xref="taxon:9913"
                        /tissue_type="pooled"
                        /lab_host="DH108"
                        /clone_lib="MARC 6BOV"
                        /notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
                        Library made with RNA pooled from multiple tissues
                        including liver, lung, hypothalamus, pituitary, and
                        placenta/endometrium."
ORIGIN
Query Match      1.9%; Score 32; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 GATCATCTCTCCAGGCGCAGCAGACGACTC 1163
      |||||||||||||||||||||||||||||||
Db 134 GATCATCTCTCCAGGCGCAGCAGACGACTC 165

RESULT 55
CW991025/c
LOCUS          260 bp mRNA linear GSS 20-JUL-2005
DEFINITION     BC0173 Sanger Institute Gene Trap Library pG72lrx Mus musculus
               cDNA, mRNA sequence.
ACCESSION      CW991025
VERSION        CW991025.3 GI:62470582
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidae; Muridae; Murinae; Mus.
               1 (bases 1 to 260)
               http://www.sanger.ac.uk/PostGenomics/genetrap/
               Unpublished (2003)
REFERENCE      On Feb 25, 2005 this sequence version replaced gi:60285534.
AUTHORS        Wellcome Trust Sanger Institute
TITLE          Email: info.genetrap@sanger.ac.uk
               Sequence tag generated by 5' RACE of total RNA from gene trap ES
               cell line. ES cell lines harboring insertion mutation of target
               gene are available upon request from Sanger Institute Gene Trap
               Resource. Annotation information available from
               http://www.sanger.ac.uk/PostGenomics/genetrap/
               Class: Gene Trap.

```

```

FEATURES     Location/Qualifiers
             source          1..260
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="129 OLA"
                        /db_xref="taxon:10090"
                        /sex="Male"
                        /cell_type="Embryonic Stem Cell"
                        /clone_lib="Sanger Institute Gene Trap Library pG72lrx"
                        /notes="Vector: pGT2lrx"
ORIGIN
Query Match      1.7%; Score 29; DB 10; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 TTCAAGAAGCTGACAGAGCTGTTTCAGCGT 758
      |||||||||||||||||||||||||||||||
Db 208 TTCAAGAAGCTGACAGAGCTGTTTCAGCGT 180

RESULT 56
CB759331
LOCUS          434 bp mRNA linear EST 16-MAY-2003
DEFINITION     AMGNNUC:NRPI4-00055-F9-A W Rat pituitary (10472) Rattus norvegicus
               cDNA clone nrpi4-00055-f9 5', mRNA sequence.
ACCESSION      CB759331
VERSION        CB759331.1 GI:29847722
KEYWORDS       EST.
SOURCE         Rattus norvegicus (Norway rat)
ORGANISM       Rattus norvegicus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidae; Muridae; Murinae; Rattus.
               1 (bases 1 to 434)
REFERENCE      Angen EST Program.
AUTHORS        Angen Rat EST Program
TITLE          Unpublished (2003)
JOURNAL        Contact: Dan Fitzpatrick
COMMENT        Angen, Inc
               One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
               Tel: 805 447-4881
               Plate: 00055 row: f column: 9.
FEATURES     Location/Qualifiers
             source          1..434
                        /organism="Rattus norvegicus"
                        /mol_type="mRNA"
                        /db_xref="taxon:10116"
                        /clone_lib="W Rat pituitary (10472)"
                        /notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat
                        pituitary adult female Wistar rat avg insert size 2.1 kb"
ORIGIN
Query Match      1.7%; Score 29; DB 6; Length 434;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 994 GACAGTGGCCATGACAGACCATGTTGGGCTC 1022
      |||||||||||||||||||||||||||||||
Db 76 GACAGTGGCCATGACAGACCATGTTGGGCTC 104

RESULT 57
BE533148
LOCUS          609 bp mRNA linear EST 09-AUG-2000
DEFINITION     601235445F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3599314 5',
               mRNA sequence.
ACCESSION      BE533148
VERSION        BE533148.1 GI:9761793
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 609)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM8781 row: 1 column: 11
High quality sequence stop: 587.

FEATURES
source

1. 609
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:359314"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match 1.7%; Score 29; DB 2; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.008; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 29; Conservative 0

QY
Db

142 AAGGACCTGGCCACCATGGCCAGAG 170
|||||
172 AAGGACCTGGCCACCATGGCCAGAG 200
|||||

RESULT 58
BI078885
LOCUS

602873115F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5005226 5',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI078885 1 GI:14497215
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
JOURNAL
COMMENT

1 (bases 1 to 738)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM1044 row: m column: 03
High quality sequence stop: 735.

FEATURES
source

1. 738
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5005226"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 1.7%; Score 29; DB 2; Length 738;
Best Local Similarity 100.0%; Pred. No. 0.0082; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 29; Conservative 0

QY
Db

142 AAGGACCTGGCCACCATGGCCAGAG 170
|||||
375 AAGGACCTGGCCACCATGGCCAGAG 403
|||||

RESULT 59
BG871324
LOCUS

602792482F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4923597 5',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BG871324 1 GI:14221864
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10845 row: c column: 22
High quality sequence start: 114
High quality sequence stop: 750.

FEATURES
source

1. 756
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4923597"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_SG2"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 1.7%; Score 29; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.0082; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 29; Conservative 0

Qy 142 AAGACCTGGCCACCATGGCCAGAG 170
 Db 216 AAGACCTGGCCACCATGGCCAGAG 244

RESULT 60
 BF041373
 LOCUS
 DEFINITION BF041373 485 bp mRNA linear EST 10-OCT-2000
 Bos taurus
 clone BP250025B20B12 5', mRNA sequence.

ACCESSION
 VERSION BF041373.1 GI:10758428
 KEYWORDS
 SOURCE EST.
 ORGANISM Bos taurus (cow)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 485)
 Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and
 Larson, J.H.

TITLE Bos taurus
 JOURNAL
 COMMENT Unpublished (2000)
 Contact: Lewin, H. A.
 W. M. Keck Center for Comparative and Functional Genomics
 University of Illinois at Urbana-Champaign
 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
 61801, USA
 Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National
 Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
 from Washington University Genome Center. Vector Trimmi g:
 Cross_match from Washington University Genome Center PHRAP suite.
 This sequence is vector free and at least 200 bp in length.

PCR primers
 FORWARD: TAATACGACTCACTATAGG
 BACKWARD: ATTAACCTCTCACTAAG
 Insert Length: 485 Std Error: 0.00
 Plate: BP250025B20 row: B column: 12
 Seq primer: AGCGATACAAATTCACAGGA
 High quality sequence stop: 485.

FEATURES
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 1..485
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="BP250025B20B12"
 /sex="female"
 /lab_host="DH10B"
 /clone_lib="Soares normalized bovine placenta"
 /note="Organ: placenta; Vector: pT73Pac; Site 1: EcoRI;
 Site 2: NotI; The cDNA library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996), Genome Research 6(9): 791-806."

ORIGIN
 Query Match 1.6%, Score 28; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 CCGCTGCTGCTGCTGGCGACCTGGGT 245
 Db 278 CCGCTGCTGCTGCTGGCGACCTGGGT 305

RESULT 61
 AL724130/c
 LOCUS
 DEFINITION AL724130 547 bp mRNA linear EST 18-APR-2002
 Danio rerio
 clone BNOAA116ZH12 5', mRNA sequence.

ACCESSION
 VERSION AL724130.1 GI:20195348
 KEYWORDS
 SOURCE EST.
 ORGANISM Danio rerio (zebrafish)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 629)
 Coimbra, R., Weil, D., Bottier, P., Blanchard, S., Levi, M.,
 Hardelin, J.P., Weissenbach, J. and Petit, C.
 A subtracted cDNA library from the zebrafish (Danio rerio)
 embryonic inner ear

TITLE Embryonic inner ear
 JOURNAL
 COMMENT Unpublished (2002)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source
 1..629
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="BNOAA116ZH12"
 /tissue_type="inner ear"
 /dev_stage="embryonic"

DEFINITION AL724130 Danio rerio embryonic inner ear subtracted cDNA Danio
 rerio cDNA clone BNOAA0732B04 5', mRNA sequence.

ACCESSION
 VERSION AL724130
 KEYWORDS
 SOURCE EST.
 ORGANISM Danio rerio (zebrafish)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 547)
 Coimbra, R., Weil, D., Bottier, P., Blanchard, S., Levi, M.,
 Hardelin, J.P., Weissenbach, J. and Petit, C.
 A subtracted cDNA library from the zebrafish (Danio rerio)
 embryonic inner ear

TITLE Embryonic inner ear
 JOURNAL
 COMMENT Unpublished (2002)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source
 1..547
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="BNOAA0732B04"
 /tissue_type="inner ear"
 /dev_stage="embryonic"
 /clone_lib="Danio rerio embryonic inner ear subtracted
 cDNA"
 /note="subtracted cDNA library"

ORIGIN
 Query Match 1.6%, Score 28; DB 1; Length 547;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1686 TTTGTAGTACCTCGCGCGACCGC 1713
 Db 31 TTTGTAGTACCTCGCGCGACCGC 4

RESULT 62
 AL730744/c
 LOCUS
 DEFINITION AL730744 629 bp mRNA linear EST 18-APR-2002
 Danio rerio
 clone BNOAA116ZH12 5', mRNA sequence.

ACCESSION
 VERSION AL730744.1 GI:20195348
 KEYWORDS
 SOURCE EST.
 ORGANISM Danio rerio (zebrafish)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 629)
 Coimbra, R., Weil, D., Bottier, P., Blanchard, S., Levi, M.,
 Hardelin, J.P., Weissenbach, J. and Petit, C.
 A subtracted cDNA library from the zebrafish (Danio rerio)
 embryonic inner ear

TITLE Embryonic inner ear
 JOURNAL
 COMMENT Unpublished (2002)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source
 1..629
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="BNOAA116ZH12"
 /tissue_type="inner ear"
 /dev_stage="embryonic"

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ORIGIN
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

Query Match      1.6%; Score 28; DB 1; Length 629;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1686 TTGTGAAGTACCTCGCGCGGACACGC 1713
DB 31 TTTGTAAGTACCTCGCGCGGACACGC 4

RESULT 63
AL715958/c
LOCUS AL715958 765 bp mRNA linear EST 18-APR-2002
DEFINITION AL715958 Danio rerio embryonic inner ear subtracted cDNA Danio
            rerio cDNA clone BN0AA011ZE08 3', mRNA sequence.
ACCESSION AL715958
VERSION AL715958.1 GI:20180561
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 765)
AUTHORS Coimbra.R., Well.D., Brottier.P., Blanchard.S., Levi.M.,
            Hardelin.J.P., Weissbach.J. and Petit.C.
TITLE A subtracted cDNA library from the zebrafish (Danio rerio)
JOURNAL
COMMENT Unpublished (2002)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..765
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA011ZE08"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN

Query Match      1.6%; Score 28; DB 1; Length 765;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1686 TTGTGAAGTACCTCGCGCGGACACGC 1713
DB 29 TTTGTAAGTACCTCGCGCGGACACGC 2

RESULT 64
CA736276
LOCUS CA736276 369 bp mRNA linear EST 26-NOV-2002
DEFINITION wpils.pk007.a7 wpils Triticum aestivum cDNA clone wpils.pk007.a7 5'
            end, mRNA sequence.
ACCESSION CA736276
VERSION CA736276.1 GI:25551874
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 369)

```

```

AUTHORS Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
TITLE DuPont Wheat cDNA Sequence
JOURNAL Unpublished (2002)
COMMENT Contact: Scott V. Tingey
            Crop Genetics
            E. I. DuPont de Nemours and Company
            1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
            Tel: 302-631-2602
            Fax: 302-631-2607
            Email: Scott.V.Tingey@USA.dupont.com
            Seq primer: M13.
            Location/Qualifiers
                1..369
                /organism="Triticum aestivum"
                /mol_type="mRNA"
                /db_xref="taxon:4565"
                /clone="wpils.pk007.a7"
                /tissue_type="leaf"
                /lab_host="DH10B"
                /clone_lib="wpils"
                /note="Vector: PGEM-T Easy; Site 1: SmaI; Wheat, Polk
                cultivar (resistant), infected with septoria tritici
                strain A 24 hours after infection"

ORIGIN

Query Match      1.6%; Score 27; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1687 TTGTGAAGTACCTCGCGCGGACACGC 1713
DB 341 TTTGTAAGTACCTCGCGCGGACACGC 367

RESULT 65
AI267255/c
LOCUS AI267255 535 bp mRNA linear EST 17-NOV-1998
DEFINITION aq62h05.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone
            IMAGE:2035545, mRNA sequence.
ACCESSION AI267255
VERSION AI267255.1 GI:3886422
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE 1 (bases 1 to 535)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
            WashU-NCI human EST Project
            Unpublished (1997)
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@wustl.edu
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -400P from Gibco
            High quality sequence stop: 442.
            Location/Qualifiers
                1..535
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2035545"
                /tissue_type="frontal lobe (see description)"
                /lab_host="DH10B (phage-resistant)"

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/clone_lib="Stanley Frontal SN pool 2"
 /notes="Organ: brain; Vector: pCR2.1-TOPO (Invitrogen);
 Site 1: EcoRI; Total RNA (purified with Trizol and DNaseI
 before use) was reverse transcribed using a modified
 oligo-dT primer containing Real and HindIII sites.
 Double-stranded cDNA was digested with Real, resulting in
 blunt ended cDNA of an average 0.1-2 kb in length.
 Digested cDNA was split into two sets, one used as is as
 the driver, the other set was split in half again and each
 half linked to a different adaptor
 (5'-TCGAGCGCGCGCGGCGGT-3' or 5'-
 AGGCGTGTGCGGAGGCGGT-3'), to be used as tester.
 Subtraction was performed using the Clontech PCR Select
 cDNA subtraction kit. Pool of two schizoprenics, male age
 44 and female age 56 (S-116, S-118) subtracted by pool of
 two mentally normal male individuals ages 41 and 53
 (S-124, S-141). Tissues were obtained from the Stanley
 Neuropathology Consortium (www.stanleylab.org). Library
 constructed and subtracted by Dr. Nancy Johnston [(410)
 614-3918, nlj@welchlink.welch.jhu.edu]."

ORIGIN

Query Match 1.6%; Score 27; DB 1; Length 535;
 Best Local Similarity 100.0%; Pred. No. 0.085;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1687 TTGTAAGTACCTCGCGCGGACACGC 1713

Db 27 TTGTAAGTACCTCGCGCGGACACGC 1

RESULT 66

LOCUS CB457332 600 bp mRNA linear EST 26-MAR-2003
 DEFINITION 714674 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION CB457332

VERSION CB457332.1 GI:29263714

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 600)

Smith, T.P.L., Roberts, A.J., Echterkamp, S.E., Chitko-McKown, C.G.,

Wray, J.E. and Keefe, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries

Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_call option. Vector identified with

cross match v0.990329.

Plate: FQY8071 row: A column: 24

Seq primer: GTAATACGACTCATATAGG.

Location/Qualifiers

1. .600

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH108"

/clone_lib="MARC 6BOV"

/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;

Library made with RNA pooled from multiple tissues

including liver, lung, hypothalamus, pituitary, and

placenta/endometrium."

ORIGIN

Query Match 1.6%; Score 27; DB 6; Length 600;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 GACTCATCTTCAGGCGGACGACACA 1158

Db 133 GACTCATCTTCAGGCGGACGACACA 159

RESULT 67

LOCUS AL718806/c

DEFINITION AL718806 Danio rerio embryonic inner ear subtracted cDNA Danio
 rerio cDNA clone BN0AA037ZE05 3', mRNA sequence.

ACCESSION AL718806

VERSION AL718806.1 GI:20183410

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 609)

Coimbra, R., Weil, D., Brottier, P., Blanchard, S., Levi, M.,

Hardelin, J.P., Weissenbach, J., and Petit, C.

A subtracted cDNA library from the zebrafish (Danio rerio)

embryonic inner ear

Unpublished (2002)

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1. .609

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="BN0AA037ZE05"

/tissue_type="inner ear"

/dev_stage="embryonic"

/clone_lib="Danio rerio embryonic inner ear subtracted

cDNA"

/note="subtracted cDNA library"

ORIGIN

Query Match 1.6%; Score 27; DB 1; Length 609;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1686 TTTGTAAGTACCTCGCGCGGACGACG 1712

Db 48 TTTGTAAGTACCTCGCGCGGACGACG 22

RESULT 68

LOCUS CX067711/c

DEFINITION CX067711 733 bp mRNA linear EST 03-JAN-2005
 ACCESSION CX067711

VERSION CX067711.1 GI:56989277

KEYWORDS EST.

SOURCE Oncorhynchus mykiss (rainbow trout)

ORGANISM Oncorhynchus mykiss

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;

Proacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 733)

Rexroad, C.B., Rise, M., Koop, B., von Schalburg, K. and Yao, J.

04RT gpool, NCCWA/WVU EST Project, Phase II, in collaboration with

GRASP

Unpublished (2004)

Contact: Rexroad CE

USDA, ARS, National Center for Cool and Cold Water Aquaculture

11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351

Email: crexroad@cccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.

Plate: 106 row: I column: 19

Seq primer: GTATATGACTTACTATAGG.

FEATURES

source
1. .733
Location/Qualifiers
/organism="Onchornychus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/lab_host="Top10"
/clone_lib="NCCCWA 04RT"
/note="Vector: PCR 4-TOPO; This is an early neurogenesis SSH library created by Mathew L. Rise constructed by subcloning late neurogenesis (mixed stages: hindbrain swelling + heart tube with peristalsis) from early neurogenesis (mixed stages: neural groove + 1/2 epiboly). Fish were from a domesticated strain (Spring Valley Trout Farm, Langley, B.C.), courtesy of Bob Devlin, DFO. These are mostly internal (coding) sequences."

ORIGIN

Query Match 1.6%; Score 27; DB 8; Length 733;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1687 TTGTAAGTACCTCGCGCGACACGC 1713

DB 33 TTGTAAGTACCTCGCGCGACACGC 7

RESULT 69

AL717228/c
LOCUS
DEFINITION AL717228 Danio rerio embryonic inner ear subcloned cDNA Danio
rerio cDNA clone BN0AA0252B11 3', mRNA sequence.

AL717228

AL717228.1 GI:20181831

EST.

SOURCE

ORGANISM

Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 738)

AUTHORS Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M.,

Hardelin,J.P., Weissenbach,J. and Petit,C.

TITLE A subcloned cDNA library from the zebrafish (Danio rerio)

JOURNAL embryonic inner ear

COMMENT Unpublished (2002)

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source
1. .738
Location/Qualifiers
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA0252B11"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subcloned cDNA"
/note="subcloned cDNA library"

ORIGIN

Query Match 1.6%; Score 27; DB 1; Length 738;
Best Local Similarity 100.0%; Pred. No. 0.088;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1687 TTGTAAGTACCTCGCGCGACACGC 1713

DB 30 TTGTAAGTACCTCGCGCGACACGC 4

RESULT 70

DN615123/c

LOCUS

DEFINITION

DN615123

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Pinus taeda (loblolly pine)
Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

REFERENCE 1 (bases 1 to 768)

AUTHORS Buell,C.R., Zheng,L., Cowles,A. and Cairney,J.

TITLE Sequencing of ESTs from loblolly pine embryonic libraries

JOURNAL Unpublished (2004)

COMMENT Contact: C. Robin Buell

Plant Genomics Group

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: rbuell@tigr.org

This clone is available through TIGR. Please contact pine@tigr.org

for further information

Seq primer: M13 forward.

FEATURES

source
1. .768
Location/Qualifiers
/organism="Pinus taeda"
/mol_type="mRNA"
/cultivar="7-56 mother tree, open-pollinated tree from, Lyons, Georgia, USA"
/db_xref="taxon:3352"
/clone="PSAC13"
/tissue_type="Whole embryos excised from megagametophytes"
/lab_host="JM109"
/clone_lib="Subtracted pine embryo library, Lib B"
/note="Organ: Zygotic Embryos; Vector: pGEM-T Easy; Site 1: EcoRI; Site 2: SpeI; Library enriched in transcripts present in early phase of loblolly pine embryo maturation. A subtractive library was made using the protocols of Clontech (Palo Alto, CA). RNA from loblolly pine embryos in which cotyledons had just emerged (Stage 9.1, see Ciavatta VT, Morillon R, Pullman GS, Chrispeels M, Cairney J. 2001. An aquaglyceroporin is abundantly expressed early in the development of the suspensor and the embryo proper of loblolly pine (Pinus taeda L.). Plant Physiol. 127: 1556-1567 [http://www.plantphysiol.org/cgi/content/full/127/4/1556]) was subtracted from RNA from pine embryos collected two weeks after cotyledon emergence (Stage 9.3)."

ORIGIN

Query Match 1.6%; Score 27; DB 8; Length 768;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1687 TTGTAAGTACCTCGCGCGACACGC 1713

DB 28 TTGTAAGTACCTCGCGCGACACGC 2

RESULT 71

BF043991

LOCUS

DEFINITION

BF043991

ACCESSION

206 bp mRNA linear EST 10-OCT-2000
BP250022B20H1 Soares normalized bovine placenta Bos taurus cDNA
clone BP250022B20H1 5', mRNA sequence.
BF043991

```

VERSION
KEYWORDS
SOURCE
ORGANISM
    Bof taurus (cow)
    Bof taurus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
    Pecora; Bovidae; Bovinae; Bos.
REFERENCE
    1 (bases 1 to 206)
AUTHORS
    Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
    Larson,J.H.
TITLE
    Bovine ESTs
JOURNAL
COMMENT
    Contact: Lewin, H. A.
    W. M. Keck Center for Comparative and Functional Genomics
    University of Illinois at Urbana-Champaign
    340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
    61801, USA
    Tel: 217 333 5998
    Fax: 217 244 5617
    Email: h-lewin@uiuc.edu
    Funding for cattle EST sequencing was provided by the USDA National
    Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
    to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
    from Washington University Genome Center. Vector Trimmi g:
    Cross_match from Washington University Genome Center PHRAP suite.
    This sequence is vector free and at least 200 bp in length.
    PCR Primers
    FORWARD: TATACGACTCCTACTAGG
    BACKWARD: ATTAACCTCTCACTAAG
    Insert Length: 206 Std Error: 0.00
    Plate: BP250022B20 row: H column: 1
    Seq primer: AGCGATAACAATTCACACAGGA
    High quality sequence stop: 206.
FEATURES
    source
    1..206
    /organism="Bos taurus"
    /mol_type="mRNA"
    /db_xref="taxon:9913"
    /clone="BP250022B20H1"
    /sex="female"
    /lab_host="DH10B"
    /clone_lib="Soares normalized bovine placenta"
    /notes="Organ: placenta; Vector: pT73Pac; Site 1: EcoRI;
    Site 2: NotI; The cDNA library was contributed by the
    Soares laboratory and it was constructed and normalized
    as described by Bonaldo, M.F., Lennon, G. and Soares,
    M.B. (1996), Genome Research 6(9): 791-806."
ORIGIN
    Query Match 1.5%; Score 26; DB 2; Length 206;
    Best Local Similarity 100.0%; Pred. No. 0.25;
    Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    1295 GAAGCAGTGCCTCTCTGGCTCTCC 1320
    Db
    59 GAAGCAGTGCCTCTCTGGCTCTCC 84

RESULT 72
CK606596
LOCUS
DEFINITION
    gmhrw6-14 C11 T7 Soybean root hair subtracted cDNA library
VERSION
    CK606596.1 GI:41146385
KEYWORDS
    Glycine max (soybean)
ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
    Glycine.
REFERENCE
    1 (bases 1 to 216)

AUTHORS
    Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.
    Expressed sequence tags from soybean root hair subtractive cDNA
    library
JOURNAL
COMMENT
    Unpublished (2003)
    Contact: Gary Stacey
    University of Missouri
    108 Waters Hall, Columbia, MO 65211, USA
    Tel: 573-884-4752
    Fax: 573-882-0588
    Email: stacey@missouri.edu
    Single pass sequence
    Seq primer: T7.
FEATURES
    Location/Qualifiers
    1..216
    /organism="Glycine max"
    /mol_type="mRNA"
    /cultivar="Williams 82"
    /db_xref="taxon:3847"
    /tissue_type="root hairs"
    /clone_lib="Soybean root hair subtracted cDNA library
    gmhrw6"
    /notes="Organ: root hairs; Vector: pGEM-T-Easy; cDNA clones
    generated from soybean root hair tissue treated with
    Bradyrhizobium japonicum for 6 hours."
ORIGIN
    Query Match 1.5%; Score 26; DB 7; Length 216;
    Best Local Similarity 100.0%; Pred. No. 0.25;
    Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    1688 TGTAAGTACTCGCGCGGACGACGC 1713
    QY
    190 TGTAAGTACTCGCGCGGACGACGC 215
    Db

RESULT 73
CA747236
LOCUS
DEFINITION
    CA747236.1 GI:25566500
    232 bp mRNA linear EST 26-NOV-2002
    wr12s.pk008.e13.f wr12s Triticum aestivum cDNA clone
    wr12s.pk008.e13.f 3' end, mRNA sequence.
ACCESSION
    CA747236
VERSION
    CA747236.1
KEYWORDS
    Triticum aestivum (bread wheat)
SOURCE
    Triticum aestivum
ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Poideae; Triticeae; Triticum.
REFERENCE
    1 (bases 1 to 232)
    Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
    Miao,G., Caraher,N. and Hanafey,M.K.
    DuPont Wheat cDNA Sequence
    Unpublished (2002)
    Contact: Scott V. Tingey
    Crop Genetics
    E. I. DuPont de Nemours and Company
    1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
    Tel: 302-631-2602
    Fax: 302-631-2607
    Email: Scott.V.Tingey@USA.dupont.com
    Seq primer: T7.
FEATURES
    Location/Qualifiers
    1..232
    /organism="Triticum aestivum"
    /mol_type="mRNA"
    /db_xref="taxon:4565"
    /clone="wr12s.pk008.e13.f"
    /tissue_type="leaf"
    /lab_host="DH10B"
    /clone_lib="wr12s"
    /notes="Vector: pGEM-T Easy; Site 1: SmaI; Riband
    (susceptible) wheat leaves infected with Septoria tritici
    strain A, 48 hours after infection, subtracted w/

```



```

ORIGIN
Query Match      1.5%; Score 26; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACTCGCGCGGACACACG 1713
|||||
Db 205 TGTAACTACTCGCGCGGACACACG 230

RESULT 74
AL726074/c
LOCUS
DEFINITION AL726074 Danio rerio embryonic inner ear subtracted cDNA Danio
rerio cDNA clone BN0AA080ZD03 5', mRNA sequence.
ACCESSION AL726074
VERSION AL726074.1 GI:20190678
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 255)
AUTHORS Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M.,
Hardelin,J.P., Weissenbach,J. and Petit,C.
TITLE A subtracted cDNA library from the zebrafish (Danio rerio)
JOURNAL embryonic inner ear
COMMENT Unpublished (2002)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .255
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA080ZD03"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/notes="subtracted cDNA library"

ORIGIN
Query Match      1.5%; Score 26; DB 1; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACTCGCGCGGACACACG 1713
|||||
Db 29 TGTAACTACTCGCGCGGACACACG 4

RESULT 75
AI267488/c
LOCUS
DEFINITION AI267488 288 bp mRNA linear EST 17-NOV-1998
IMAGE:01.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone
IMAGE:2035800, mRNA sequence.
ACCESSION AI267488
VERSION AI267488.1 GI:3886655
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 288)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,

comparable uninfected leaves"

TITLE
JOURNAL
COMMENT

Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,P.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 287.
Location/Qualifiers
1. .288
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2035800"
/tissue_type="frontal lobe (see description)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Stanley Frontal SN pool 2"
/notes="Organ: brain; Vector: pCR2.1-TOPO (Invitrogen);
Site 1: EcoRI; Total RNA (purified with Trizol and DNaseI
before use) was reverse transcribed using a modified
oligo-dT primer containing RsaI and HindIII sites.
Double- stranded cDNA was digested with RsaI, resulting in
blunt ended cDNA of an average 0.1-2 kb in length.
Digested cDNA was split into two sets, one used as is as
the driver, the other set was split in half again and each
half linked to a different adaptor
(5'-TCGAGCGCGCGCGGCGGAGT-3' or 5'-
ACGGCGTGTGCGGAGCGCGGT-3'), to be used as tester.
Subtraction was performed using the Clontech PCR Select
cDNA subtraction kit. Pool of two schizoprenics, male age
44 and female age 56 (S-116, S-118) subtracted by pool of
two mentally normal male individuals ages 41 and 53
(S-124, S-141). Tissues were obtained from the Stanley
Neuropathology Consortium (www.stanleylab.org). Library
constructed and subtracted by Dr. Nancy Johnston [(410)
614-3918, nlj@weichlink.weich.jhu.edu]."
```

E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.

FEATURES

source
Location/Qualifiers
1. .344
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wp1s.pk002.e11"
/tissue_type="leaf"
/lab_host="DH10B"
/clone_lib="wp1s"
/notes="Vector: pGEM-T Easy; Site 1: SmaI; Wheat, Polk cultivar (resistant), infected with septoria tritici strain A 24 hours after infection"

Query Match 1.5%; Score 26; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1688 TGTAACTACCTCGCGCGACCGC 1713
|||||
DB 28 TGTAACTACCTCGCGCGACCGC 3

RESULT 77

AW481164
LOCUS AW481164 402 bp mRNA linear EST 25-APR-2001
DEFINITION 34685 MARC 1B0V Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW481164
VERSION AW481164.1 GI:7051270
KEYWORDS EST.
SOURCE Bos taurus (cow)

ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS Smith,T.P.L., Grosse,W.M., Preking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKown,C.G., Perlea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

11282978

CONTACT: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 20

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTTCCAGTCACGACG

Plate: 18 row: G column: 24

Seq primer: ATTAGTGACACTATAG.

Location/Qualifiers

1. .402

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 1B0V"

ORIGIN

Query Match 1.5%; Score 26; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 GGGCTGCCTTCTGCTTCGCGCGCTGC 285
|||||
DB 81 GGGCTGCCTTCTGCTTCGCGCGCTGC 106

ORIGIN

Query Match 1.5%; Score 26; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1295 GAAGCAGTGCCCACTCTGGCTCTCC 1320
|||||
DB 68 GAAGCAGTGCCCACTCTGGCTCTCC 93

RESULT 78

BF150866
LOCUS BF150866 425 bp mRNA linear EST 29-DEC-2000
DEFINITION uy88g10.y1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3666690 5', mRNA sequence.

ACCESSION BF150866

VERSION BF150866.1 GI:11032261

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS 1 (bases 1 to 425)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

TITLE

Tumor Gene Index

Unpublished (1997)

Other ESTs: uy88g10.x1

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

image.lnl.gov/image/html/iresources.shtml

MGI:1427458

Seq primer: -40RP from Gibco

High quality sequence stop: 395.

FEATURES

source

1. .425

/organism="Mus musculus"

/mol_type="mRNA"

/strain="mix FVB/N, C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:3666690"

/tissue_type="tumor, gross tissue"

/dev_stage="7 months"

/lab_host="DH10B"

/clone_lib="NCI CGAP Mam5"

/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Robin Humphreys,

NIH"

RESULT 79
AW762557 426 bp mRNA linear EST 04-MAY-2000
LOCUS ur57f12.y1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:3154415 5',
DEFINITION mRNA sequence.
ACCESSION AW762557
VERSION AW762557.1 GI:7694486
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 426)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other ESTs: ur57f12.x1
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
MGI:1057171
Seq primer: -4ORP from Gibco
High quality sequence stop: 422.
FEATURES
source
1. .426
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129, C57BL/6J, FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3154415"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
ORIGIN
Query Match 1.5%; Score 26; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 487 GATGTTAAGCTCAAGGCATCCCTGT 512
Db 227 GATGTTAAGCTCAAGGCATCCCTGT 252
RESULT 80
CB732455 475 bp mRNA linear EST 11-APR-2003
LOCUS AMGNNUC:SRCS1-00007-E10-A srcs1 (10883) Rattus norvegicus cDNA
DEFINITION clone srcs1-00007-e10 5', mRNA sequence.
ACCESSION CB732455
VERSION CB732455.1 GI:29799612
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 475)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00007 row: e column: 10.
FEATURES
source
1. .475
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="srcs1-00007-e10"
/tissue_type="Cornea"
/clone_lib="srcs1 (10883)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Site_2: EcoRI;
rat corneas"
ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 475;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1688 TGTAACTACTCGCGCGACCAACGC 1713
Db 450 TGTAACTACTCGCGCGACCAACGC 475
RESULT 81
CA882810/c 485 bp mRNA linear EST 20-DEC-2002
LOCUS SSHD160 Rice callus and differential tissue SSH library Oryza
DEFINITION sativa cDNA, mRNA sequence.
ACCESSION CA882810
VERSION CA882810.1 GI:27334359
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 485)
AUTHORS Du, X., Wang, D. and Yang, J.
TITLE Rice cDNA from callus (2002)
JOURNAL Unpublished (2002)
COMMENT Contact: DU Xiling
Institute of Genetics, Fudan University
Handan Road 220, Shanghai 200433, China
Tel: 86-21-6564-3715
Email: dxiling@yahoo.com.cn.
FEATURES
source
1. .485
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Wuyunjing No. 7"
/db_xref="taxon:4530"
/clone_lib="Rice callus and differential tissue SSH
library"
/note="Vector: pGEM-T; suppressed subtract hybridized
cDNA prepared from rice callus mRNAs
ligating to
pGEM-T"
ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1688 TGTAACTACTCGCGCGACCAACGC 1713
Db 81 TGTAACTACTCGCGCGACCAACGC 56

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RESULT 82
CF036397/c
LOCUS
DEFINITION QCG30h07.yg QCG Zea mays cDNA clone QCG30h07, mRNA sequence. EST 17-JUL-2003
ACCESSION CF036397
VERSION CF036397.1 GI:32931585
KEYWORDS
SOURCE
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 501)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.
FEATURES
source
location/Qualifiers
1..501
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="P2"
/db_xref="taxon:4577"
/clone="QCG30h07"
/tissue_type="embryo"
/clone_lib="QCG"
ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1688 TGTAACTACCTCGCGCGGACCGC 1713
|||||
DB 28 TGTAACTACCTCGCGCGGACCGC 3
|||||
RESULT 83
AL720496/c
LOCUS
DEFINITION AL720496 Danio rerio embryonic inner ear subtracted cDNA Danio
rerio cDNA clone BN0AA0482B03 3', mRNA sequence.
ACCESSION AL720496
VERSION AL720496.1 GI:20185100
KEYWORDS
SOURCE
ORGANISM Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 520)
Coimbra.R., Weil.D., Brottier.P., Blanchard.S., Levi.M.,
Hardein.J.P., Weissenbach.J. and Petit.C.
A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
Unpublished (2002)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1..520
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
FEATURES
source
```

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/clone="BN0AA0482B03"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/notes="subtracted cDNA library"
ORIGIN
Query Match 1.5%; Score 26; DB 1; Length 520;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1688 TGTAACTACCTCGCGCGGACCGC 1713
|||||
DB 29 TGTAACTACCTCGCGCGGACCGC 4
|||||
RESULT 84
AI267373/c
LOCUS
DEFINITION aiq64C09.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone
IMAGE:2035696, mRNA sequence.
ACCESSION AI267373
VERSION AI267373.1 GI:3886540
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 543)
Hillier.L., Allen.M., Bowles.L., Dubuque.T., Geisels.G., Jost.S.,
Krizman.D., Kucaba.T., Lacy.M., Lennon.G., Marra.M.,
Martin.J., Moore.B., Schellenberg.K., Steptoe.M., Tan.F.,
Theising.B., White.Y., Wylie.T., Waterston.R. and Wilson.R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 437.
FEATURES
source
location/Qualifiers
1..543
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2035696"
/tissue_type="frontal lobe (see description)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Stanley Frontal SN pool 2"
/notes="Organ: brain; Vector: pCR2.1-TOPO (Invitrogen);
Site 1: EcoRI; Total RNA (purified with Trizol and DNaseI
before use) was reverse transcribed using a modified
oligo-dT primer containing Real and HindIII sites.
Double- stranded cDNA was digested with Real, resulting in
blunt ended cDNA of an average 0.1-2 kb in length.
Digested cDNA was split into two sets, one used as is as
the driver, the other set was split in half again and each
half linked to a different adaptor
(5'-TCGAGCGCGCGCGGAGGT-3' or 5'-
AGGCGGTGTGCGGAGCGGT-3') to be used as tester.
Subtraction was performed using the Clontech PCR Select
cDNA subtraction kit. Pool of two schizophrenics, male age
44 and female age 56 (S-116, S-118) subtracted by pool of
two mentally normal male individuals ages 41 and 53
(S-124, S-141). Tissues were obtained from the Stanley
Neuropathology Consortium (www.stanleylab.org). Library
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constructed and subtracted by Dr. Nancy Johnston [(410)
614-3918, nlj@welchlink.welch.jhu.edu]."
```

ORIGIN

Query Match 1.5%; Score 26; DB 1; Length 543;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACTCGCGCGGACACCGC 1713
|||||
DB 26 TGTAACTACTCGCGCGGACACCGC 1

RESULT 85
CB464871/C

LOCUS 726118 MARC 6BOV Bos taurus cDNA 3', mRNA linear EST 26-MAR-2003
DEFINITION CB464871
ACCESSION
VERSION CB464871.1 GI:29271256
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 547)
AUTHORS Smith,T.P.L., Roberts,A.J., Ehternkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.

TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: LAM8004 row: M column: 8
Seq primer: TAGAGGACACAGTCGAGG.

FEATURES
Location/Qualifiers
source 1..547
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

ORIGIN

Query Match 1.5%; Score 26; DB 6; Length 547;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1295 GAAGCAGTGCCTCTGGCTCTCTCC 1320
|||||
DB 474 GAAGCAGTGCCTCTGGCTCTCTCC 449

RESULT 86
AL714240/C

LOCUS AL714240
DEFINITION AL714240 Danio rerio embryonic inner ear subtracted cDNA Danio
rerio cDNA clone BN0AA003ZC08 5', mRNA linear EST 18-APR-2002
ACCESSION AL714240
VERSION AL714240.1 GI:20178843
KEYWORDS
SOURCE Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 557)
AUTHORS Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M.,
Hardelin,J.P., Weissenbach,J. and Petit,C.

TITLE A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
JOURNAL Unpublished (2002)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Location/Qualifiers
source 1..557
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA003ZC08"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN

Query Match 1.5%; Score 26; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACTCGCGCGGACACCGC 1713
|||||
DB 29 TGTAACTACTCGCGCGGACACCGC 4

RESULT 87
AL714414

LOCUS AL714414
DEFINITION AL714414 Danio rerio embryonic inner ear subtracted cDNA Danio
rerio cDNA clone BN0AA005ZH12 5', mRNA linear EST 18-APR-2002
ACCESSION AL714414
VERSION AL714414.1 GI:20179017
KEYWORDS
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 557)
AUTHORS Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M.,
Hardelin,J.P., Weissenbach,J. and Petit,C.

TITLE A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
JOURNAL Unpublished (2002)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Location/Qualifiers
source 1..557
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA005ZH12"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN

Query Match 1.5%; Score 26; DB 1; Length 557;

Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAAAGTACCTCGCGCGGACACGC 1713
Db 531 TGTAAAGTACCTCGCGCGGACACGC 556

RESULT 88
AL714437/c
LOCUS
DEFINITION AL714437 Danio rerio embryonic inner ear subtracted cDNA Danio
Accession AL714437 558 bp mRNA linear EST 18-APR-2002
Version AL714437.1 GI:20179040
Keywords
Source
Organism Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
Reference 1 (bases 1 to 558)
Authors Coimbra.R., Weil.D., Brottier.P., Blanchard.S., Levi.M.,
Hardelin.J.P., Weissenbach.J. and Petit.C.
Title A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
Journal Unpublished (2002)
Comment Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 558
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA005ZH12"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN
Query Match 1.5%; Score 26; DB 1; Length 558;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAAAGTACCTCGCGCGGACACGC 1713
Db 531 TGTAAAGTACCTCGCGCGGACACGC 556

RESULT 89
AL714276/c
LOCUS
DEFINITION AL714276 Danio rerio embryonic inner ear subtracted cDNA Danio
Accession AL714276 561 bp mRNA linear EST 18-APR-2002
Version AL714276.1 GI:20178879
Keywords
Source
Organism Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
Reference 1 (bases 1 to 561)
Authors Coimbra.R., Weil.D., Brottier.P., Blanchard.S., Levi.M.,
Hardelin.J.P., Weissenbach.J. and Petit.C.
Title A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
Journal Unpublished (2002)
Comment Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 561
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA003ZC08"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN
Query Match 1.5%; Score 26; DB 1; Length 572;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAAAGTACCTCGCGCGGACACGC 1713
Db 29 TGTAAAGTACCTCGCGCGGACACGC 4

RESULT 91
CF064307/c
LOCUS

Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 561
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA003ZC08"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN
Query Match 1.5%; Score 26; DB 1; Length 561;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAAAGTACCTCGCGCGGACACGC 1713
Db 533 TGTAAAGTACCTCGCGCGGACACGC 558

RESULT 90
AL716984/c
LOCUS
DEFINITION AL716984 Danio rerio embryonic inner ear subtracted cDNA Danio
Accession AL716984 572 bp mRNA linear EST 18-APR-2002
Version AL716984.1 GI:20181587
Keywords
Source
Organism Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
Reference 1 (bases 1 to 572)
Authors Coimbra.R., Weil.D., Brottier.P., Blanchard.S., Levi.M.,
Hardelin.J.P., Weissenbach.J. and Petit.C.
Title A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
Journal Unpublished (2002)
Comment Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 572
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA021ZA01"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN
Query Match 1.5%; Score 26; DB 1; Length 572;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAAAGTACCTCGCGCGGACACGC 1713
Db 29 TGTAAAGTACCTCGCGCGGACACGC 4

RESULT 91
CF064307/c
LOCUS

```

DEFINITION   QCU9g04.yg QCU Zea mays cDNA clone QCU9g04, mRNA sequence.
ACCESSION    CF064307
VERSION      CF064307.1 GI:33104347
KEYWORDS     EST.
SOURCE       Zea mays
ORGANISM     Zea mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE    1 (bases 1 to 581)
AUTHORS      Genoplante.
TITLE        Genoplante, a major partnership french program in plant genomics
JOURNAL      Unpublished (2003)
COMMENT      Contact: Genoplante
              93, rue Henri Rochefort 91025 EVRY CEDEX France
              Tel: 33 1 69 47 54 00
              Fax: 33 1 69 47 54 10
              This sequence has been generated in the framework of the french
              plant genomics programme 'genoplante' (http://www.genoplante.com
              and http://genoplante-info.infobiogen.fr).
FEATURES     Location/Qualifiers
              source          1..581
                           /organism="Zea mays"
                           /mol_type="mRNA"
                           /culturav="f333 or f334"
                           /db_xref="taxon:4577"
                           /clone="QCU9g04"
                           /tissue type="seedling minus kernel"
                           /clone_lib="QCU"
ORIGIN
Query Match      1.5%; Score 26; DB 6; Length 581;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1688 TGTAACTACTCGCGCGACACG 1713
|||||
Db 28 TGTAACTACTCGCGCGACACG 3

RESULT 92
BY753126
LOCUS
DEFINITION     BY753126 RIKEN full-length enriched, adult inner ear Mus musculus
ACCESSION      BY753126
VERSION        BY753126.1 GI:27184397
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
              Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 657)
AUTHORS        Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
              Nikaido,I., Oatono,M., Saito,R., Suzuki,H., Yamanaka,I.,
              Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
              Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
              Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
              Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
              Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
              Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,I.,
              Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
              Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
              Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
              Kurochkin,I.V., Lee,V., Lenhard,B., Lyons,P.A., Maglott,D.R.,
              Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
              Numata,K., Okido,T., Pavan,W.J., Perte,G., Pesole,G.,
              Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
              Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
              Sandelin,A., Schneider,C., Sempile,C.A., Setou,M., Shimada,K.,
              Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,

```

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Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wyshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yaunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Wataniki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Kirk W. Beisel ( Boys Town National
Research Hospital 555 North 30th Street Omaha,NE 68131 USA ) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES     Location/Qualifiers
              source          1..657
                           /organism="Mus musculus"
                           /mol_type="mRNA"
                           /strain="C57BL/6J"
                           /db_xref="taxon:10090"
                           /clone="F930111008"
                           /tissue_type="inner ear"
                           /div_stage="adult"
                           /clone_lib="RIKEN full-length enriched, adult inner ear"
ORIGIN
Query Match      1.5%; Score 26; DB 5; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 GGGCTGCCTTCGCTTCGCCGCGCTGC 285
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Db 524 GGGCTGCCTTCGCTTCGCCGCGCTGC 549

RESULT 93
BI653517

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LOCUS       BI653517               680 bp      mRNA      linear      EST 12-SEP-2001
DEFINITION  603300520F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5341085 5',
mRNA sequence.
ACCESSION   BI653517
VERSION     BI653517.1  GI:15567753
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 680)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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FEATURES             source
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         /db_xref="taxon:10090"
         /clone="IMAGE:5341085"
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         /dev_stage="10 months"
         /lab_host="DH10B"
         /clone_lib="NCI_CGAP_Mam3"
         /notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali;
            Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
            Library constructed by Life Technologies. Investigators
            providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
            Reference for transgenic model: Xu et al., Nature Genetics
            22, 37-43 (1999)."
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ORIGIN
Query Match      1.5%; Score 26; DB 3; Length 680;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  260 GGCTGCTTCTGCTTCGCGCGCTGC 285
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Db   524 GGCTGCTTCTGCTTCGCGCGCTGC 549

RESULT 95
DN478595/c
LOCUS       DN478595               692 bp      mRNA      linear      EST 09-MAR-2005
DEFINITION  alt010xm17 A. brassicicola mycelial culture infecting B. oleracea
mRNA sequence.
ACCESSION   DN478595
VERSION     DN478595.1  GI:60675906
KEYWORDS    EST.
SOURCE      Alternaria brassicicola
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
            Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.
REFERENCE   1  (bases 1 to 692)
AUTHORS     Cramer,R.A., Craven,K.D., Thon,M.R., Cho,Y., Knudson,D.L.,
            Mitchell,T.K. and Lawrence,C.B.
TITLE       Expressed Sequence Tag (EST) Analysis of a Compatible Alternaria
            brassicicola-Brassica oleracea interaction
JOURNAL     Unpublished (2005)
COMMENT     Contact: Dr. Thomas K. Mitchell
            Center for Integrated Fungal Research, NC State University
            851 Main Campus Dr. Suite 233, Raleigh, NC 27606, USA
            Tel: (919) 513-3926
            Fax: (919) 513-0024
            Email: thomas_mitchell@ncsu.edu
            Seq primer: T7 SP6 primer.

FEATURES             source
     source
     1..692
         /organism="Alternaria brassicicola"
         /mol_type="mRNA"
         /strain="ATCC 96866"
         /db_xref="taxon:29001"
         /clone="alt010xm17"
         /dev_stage="mycelia"
         /clone_lib="A. brassicicola mycelial culture infecting B.
            oleracea"
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```

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1092 Row: f column: 10
High quality sequence stop: 685.

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         /notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali;
            Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
            Library constructed by Life Technologies. Investigators
            providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
            Reference for transgenic model: Xu et al., Nature Genetics
            22, 37-43 (1999)."
```

```

24 degrees C, minimal media minus Nitrogen. Infecting
Brassica oleracea Var. Capitata cultivar 'tenderwestfl'"

ORIGIN

Query Match      1.5%; Score 26; DB 8; Length 692;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAAGTACTCGGCGCGACCAACGC 1713
    |||||
Db 28 TGTAAGTACTCGGCGCGACCAACGC 3

RESULT 96
CV943849
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytophthora infestans (potato late blight agent)
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE
AUTHORS
1 (bases 1 to 707)
Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
Lam,S.T., and Judelson, H.S.
Large-scale gene discovery in the oomycete Phytophthora infestans
reveals likely components of phytopathogenicity shared with true
fungi
JOURNAL
PUBMED
15782637
COMMENT
Contact: Judelson HS
Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
Location/Qualifiers
FEATURES
source
1..707
/organism="Phytophthora infestans"
/mol_type="mRNA"
/strain="88069"
/db_xref="taxon:4787"
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/clone_lib="mycelium, subtracted infection mimic"
/note="Vector: pSPORT1"

ORIGIN

Query Match      1.5%; Score 26; DB 8; Length 707;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAAGTACTCGGCGCGACCAACGC 1713
    |||||
Db 287 TGTAAGTACTCGGCGCGACCAACGC 312

RESULT 97
BI409054
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 722)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11284 row: e column: 05
High quality sequence stop: 720.
Location/Qualifiers
1..722
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/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI CGAP Lu33"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAATGGAGCGCGCTCTGTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match      1.5%; Score 26; DB 3; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 GGGCTGCCCTTCGCTTCGCGCGCTGC 285
    |||||
Db 440 GGGCTGCCCTTCGCTTCGCGCGCTGC 465

RESULT 98
CV944323
LOCUS
DEFINITION
infestans cDNA, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytophthora infestans (potato late blight agent)
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
1 (bases 1 to 737)
Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
Lam,S.T., and Judelson, H.S.
Large-scale gene discovery in the oomycete Phytophthora infestans
reveals likely components of phytopathogenicity shared with true
fungi

TITLE

```

JOURNAL
FURNED
COMMENT

Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
15782637
Contact: Judelson HS
Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
Email: howard.judelson@ucr.edu.

FEATURES

source
1. .737
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/organism="Phytophthora infestans"
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/note="vector: pSPORT1"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1688 TGTAACTACCTCGCCCGACCGC 1713

Db 305 TGTAACTACCTCGCCCGACCGC 330

RESULT 99

BI159562
LOCUS 746 bp mRNA linear EST 05-JUL-2001
DEFINITION 602919525F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5059854 5', mRNA sequence.

ACCESSION BI159562.1 GI:14619563

VERSION

KEYWORDS Mus musculus (house mouse)

SOURCE

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 746)

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM1162 row: a column: 07

High quality sequence start: 3

High quality sequence stop: 742.

FEATURES

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/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam3"

/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI. Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH

ORIGIN

Query Match 1.5%; Score 26; DB 2; Length 746;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 GGGCTGCTTCTGCTTCGCCGCTGC 285

Db 517 GGGCTGCTTCTGCTTCGCCGCTGC 542

RESULT 100

BI905713
LOCUS 746 bp mRNA linear EST 16-OCT-2001
DEFINITION 603166180F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5254507 5', mRNA sequence.

ACCESSION BI905713.1 GI:16168280

VERSION

KEYWORDS Mus musculus (house mouse)

SOURCE

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 746)

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11642 row: o column: 20

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High quality sequence stop: 746.

FEATURES

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/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI CGAP Lu33"
/notes="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5', TGTACCAATCTGAAGTGGAGCGCGCTCTGTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatimaonaldo."

ORIGIN

Query Match 1.5%; Score 26; DB 3; Length 746;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 GGGCTGCTTCTGCTTCGCCGCTGC 285

Db 420 GGGCTGCTTCTGCTTCGCCGCTGC 445

Search completed: March 11, 2006, 23:47:04
Job time : 6327 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 20:34:24 ; Search time 325 Seconds
(without alignments)
9369.117 Million cell u

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Title:      US-09-989-890-105
Perfect score: 1713
Sequence:   1 atgccccgccctggacacc.....tacctcggccgcgaccacgc 1713

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Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

word size : 0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

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7: /cgn2_6/ptodata/1/lna/PPR COMB.seq.*
8: /cgn2_6/ptodata/1/lna/RE COMB.seq.*
9: /cgn2_6/ptodata/1/lna/backfileal.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1594	93.1	1785	3	US-10-104-047-799	Sequence 799, App
2	25	1.5	224	3	US-10-131-827-8473	Sequence 8473, Ap
3	23	1.3	170	3	US-10-131-827-8150	Sequence 8150, Ap
C 4	23	1.3	468	3	US-09-328-475C-111	Sequence 111, App
C 5	23	1.3	482	3	US-09-328-475C-346	Sequence 246, App
C 6	23	1.3	483	3	US-09-328-475C-239	Sequence 239, App
C 7	23	1.3	493	3	US-09-328-475C-324	Sequence 224, App
C 8	23	1.3	499	3	US-09-328-475C-185	Sequence 185, App
C 9	23	1.3	501	3	US-09-328-475C-181	Sequence 181, App
C 10	23	1.3	511	3	US-09-328-475C-196	Sequence 196, App
C 11	23	1.3	719	3	US-09-328-475C-305	Sequence 305, App
C 12	23	1.3	722	3	US-09-328-475C-315	Sequence 315, App
C 13	23	1.3	724	3	US-09-328-475C-277	Sequence 277, App
C 14	23	1.3	725	3	US-09-328-475C-295	Sequence 295, App
C 15	23	1.3	725	3	US-09-328-475C-329	Sequence 329, App
C 16	23	1.3	727	3	US-09-328-475C-331	Sequence 331, App
C 17	23	1.3	736	3	US-09-328-475C-294	Sequence 294, App
C 18	23	1.3	740	3	US-09-328-475C-314	Sequence 314, App
C 19	23	1.3	741	3	US-09-328-475C-304	Sequence 304, App
C 20	23	1.3	741	3	US-09-328-475C-330	Sequence 330, App
C 21	23	1.3	744	3	US-09-328-475C-276	Sequence 276, App
C 22	23	1.3	747	3	US-09-328-475C-328	Sequence 328, App
C 23	23	1.3	772	3	US-09-328-475C-158	Sequence 158, App
C 24	23	1.3	780	3	US-09-328-475C-153	Sequence 153, App

98	21	1.2	301	3	US-10-012-896-293	Sequence 293, App	C 171	21	1.2	815	3	US-09-328-475C-118	Sequence 118, App
99	21	1.2	311	3	US-10-131-827-8546	Sequence 8546, Ap	C 172	21	1.2	815	3	US-09-328-475C-227	Sequence 227, App
C 100	21	1.2	378	3	US-09-188-930-71	Sequence 71, App1	C 173	21	1.2	817	3	US-09-328-475C-231	Sequence 231, App
C 101	21	1.2	378	3	US-09-312-283C-71	Sequence 71, App1	C 174	21	1.2	819	3	US-09-328-475C-203	Sequence 203, App
C 102	21	1.2	413	3	US-09-188-930-55	Sequence 55, App1	C 175	21	1.2	823	3	US-09-328-475C-180	Sequence 180, App
C 103	21	1.2	413	3	US-09-312-283C-55	Sequence 55, App1	C 176	21	1.2	824	3	US-09-328-475C-184	Sequence 184, App
C 104	21	1.2	467	3	US-09-328-475C-122	Sequence 122, App	C 177	21	1.2	824	3	US-09-328-475C-243	Sequence 243, App
C 105	21	1.2	471	3	US-09-328-475C-115	Sequence 115, App	C 178	21	1.2	827	3	US-09-328-475C-217	Sequence 217, App
C 106	21	1.2	474	3	US-09-328-475C-235	Sequence 235, App	C 179	21	1.2	831	3	US-09-328-475C-221	Sequence 221, App
C 107	21	1.2	480	3	US-10-131-827-8654	Sequence 8654, Ap	C 180	21	1.2	831	3	US-09-328-475C-253	Sequence 253, App
C 108	21	1.2	481	3	US-09-328-475C-250	Sequence 250, App	C 181	21	1.2	833	3	US-09-328-475C-125	Sequence 125, App
C 109	21	1.2	494	3	US-10-131-827-8604	Sequence 8604, Ap	C 182	21	1.2	840	3	US-09-328-475C-204	Sequence 204, App
C 110	21	1.2	495	3	US-09-328-475C-209	Sequence 209, App	C 183	21	1.2	950	3	US-09-328-475C-138	Sequence 138, App
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C 112	21	1.2	497	3	US-09-328-475C-203	Sequence 203, App	C 185	21	1.2	1007	3	US-09-328-475C-106	Sequence 106, App
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C 115	21	1.2	502	3	US-09-328-475C-230	Sequence 230, App	C 188	21	1.2	1024	3	US-09-328-475C-46	Sequence 46, App1
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C 118	21	1.2	524	3	US-09-328-475C-256	Sequence 256, App	C 191	21	1.2	1024	3	US-09-328-475C-59	Sequence 59, App1
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C 123	21	1.2	703	3	US-09-339-338-66	Sequence 66, App1	C 196	21	1.2	1024	3	US-09-328-475C-70	Sequence 70, App1
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245	20	1.2	844	3	US-10-076-622-77	Sequence 76, Appl	318	1.1	181	3	US-09-389-681-119	Sequence 119, App
246	20	1.2	72704	3	US-09-902-540-1273	Sequence 1273, Ap	319	1.1	181	3	US-09-620-405B-119	Sequence 119, App
247	19	1.1	20	3	US-09-284-782-11	Sequence 11, Appl	320	1.1	181	3	US-09-339-338-119	Sequence 119, App
248	19	1.1	20	3	US-09-323-873A-27	Sequence 27, Appl	321	1.1	181	3	US-09-433-826B-119	Sequence 119, App
249	19	1.1	20	3	US-09-455-486-29	Sequence 29, Appl	322	1.1	181	3	US-09-604-287A-119	Sequence 119, App
250	19	1.1	20	3	US-10-027-807-7	Sequence 7, Appl	323	1.1	181	3	US-09-285-480-119	Sequence 119, App
251	19	1.1	20	3	US-10-027-807-10	Sequence 10, Appl	324	1.1	181	3	US-09-834-759-119	Sequence 119, App
252	19	1.1	20	3	US-10-027-807-13	Sequence 13, Appl	325	1.1	181	3	US-09-590-751A-119	Sequence 119, App
253	19	1.1	20	3	US-10-027-807-16	Sequence 16, Appl	326	1.1	181	3	US-09-551-621-119	Sequence 119, App
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262	19	1.1	26	3	US-09-338-933-242	Sequence 242, App	c 335	1.1	192	3	US-09-285-480-91	Sequence 91, Appl
263	19	1.1	26	3	US-09-215-681-242	Sequence 242, App	c 336	1.1	192	3	US-09-834-759-91	Sequence 91, Appl
264	19	1.1	26	3	US-09-216-003A-242	Sequence 242, App	c 337	1.1	192	3	US-09-590-751A-91	Sequence 91, Appl
265	19	1.1	26	3	US-09-667-857-242	Sequence 242, App	c 338	1.1	192	3	US-09-551-621-91	Sequence 91, Appl
266	19	1.1	26	3	US-10-198-053-242	Sequence 242, App	c 339	1.1	192	3	US-09-551-621A-91	Sequence 91, Appl
267	19	1.1	26	3	US-09-827-271-242	Sequence 242, App	c 340	1.1	192	3	US-10-076-622-91	Sequence 91, Appl
268	19	1.1	42	3	US-09-323-873A-24	Sequence 24, Appl	c 341	1.1	199	3	US-09-222-575-125	Sequence 125, App
269	19	1.1	42	3	US-09-455-486-25	Sequence 25, Appl	c 342	1.1	199	3	US-09-389-681-125	Sequence 125, App
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279	19	1.1	72	3	US-09-667-857-304	Sequence 304, App	c 352	1.1	199	3	US-10-076-622-125	Sequence 125, App
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281	19	1.1	72	3	US-09-827-271-304	Sequence 304, App	c 354	1.1	204	3	US-09-401-064-66	Sequence 66, Appl
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283	19	1.1	91	3	US-09-338-933-201	Sequence 201, App	c 356	1.1	208	3	US-09-404-879A-231	Sequence 231, App
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292	19	1.1	101	3	US-09-216-003A-293	Sequence 293, App	c 365	1.1	208	3	US-10-198-053-230	Sequence 230, App
293	19	1.1	101	3	US-09-667-857-293	Sequence 293, App	c 366	1.1	208	3	US-10-198-053-231	Sequence 231, App
294	19	1.1	101	3	US-10-198-053-293	Sequence 293, App	c 367	1.1	208	3	US-09-827-271-230	Sequence 230, App
295	19	1.1	101	3	US-09-827-271-293	Sequence 293, App	c 368	1.1	208	3	US-09-827-271-231	Sequence 231, App
296	19	1.1	148	3	US-09-404-879A-185	Sequence 185, App	c 369	1.1	212	3	US-09-404-879A-319	Sequence 319, App
297	19	1.1	148	3	US-09-338-933-185	Sequence 185, App	c 370	1.1	212	3	US-09-667-857-319	Sequence 319, App
298	19	1.1	148	3	US-09-215-681-185	Sequence 185, App	c 371	1.1	212	3	US-10-198-053-319	Sequence 319, App
299	19	1.1	148	3	US-09-216-003A-185	Sequence 185, App	c 372	1.1	212	3	US-09-827-271-319	Sequence 319, App
300	19	1.1	148	3	US-09-667-857-185	Sequence 185, App	c 373	1.1	223	3	US-09-222-575-96	Sequence 96, Appl
301	19	1.1	148	3	US-10-198-053-185	Sequence 185, App	c 374	1.1	223	3	US-09-389-681-96	Sequence 96, Appl
302	19	1.1	148	3	US-09-827-271-185	Sequence 185, App	c 375	1.1	223	3	US-09-620-405B-96	Sequence 96, Appl
303	19	1.1	170	3	US-09-221-298-57	Sequence 57, Appl	c 376	1.1	223	3	US-09-339-338-96	Sequence 96, Appl
304	19	1.1	170	3	US-09-401-064-57	Sequence 57, Appl	c 377	1.1	223	3	US-09-433-826B-96	Sequence 96, Appl
305	19	1.1	174	3	US-09-222-575-122	Sequence 122, App	c 378	1.1	223	3	US-09-604-287A-96	Sequence 96, Appl
306	19	1.1	174	3	US-09-389-681-122	Sequence 122, App	c 379	1.1	223	3	US-09-285-480-96	Sequence 96, Appl
307	19	1.1	174	3	US-09-620-405B-122	Sequence 122, App	c 380	1.1	223	3	US-09-834-759-96	Sequence 96, Appl
308	19	1.1	174	3	US-09-339-338-122	Sequence 122, App	c 381	1.1	223	3	US-09-590-751A-96	Sequence 96, Appl
309	19	1.1	174	3	US-09-433-826B-122	Sequence 122, App	c 382	1.1	223	3	US-09-551-621-96	Sequence 96, Appl
310	19	1.1	174	3	US-09-604-287A-122	Sequence 122, App	c 383	1.1	223	3	US-09-551-621A-96	Sequence 96, Appl
311	19	1.1	174	3	US-09-285-480-122	Sequence 122, App	c 384	1.1	223	3	US-10-076-622-96	Sequence 96, Appl
312	19	1.1	174	3	US-09-834-759-122	Sequence 122, App	c 385	1.1	226	3	US-09-404-879A-79	Sequence 79, Appl
313	19	1.1	174	3	US-09-590-751A-122	Sequence 122, App	c 386	1.1	226	3	US-09-404-879A-233	Sequence 233, App
314	19	1.1	174	3	US-09-551-621-122	Sequence 122, App	c 387	1.1	226	3	US-09-404-879A-254	Sequence 254, App
315	19	1.1	174	3	US-09-551-621A-122	Sequence 122, App	c 388	1.1	226	3	US-09-338-933-79	Sequence 79, Appl
316	19	1.1	174	3	US-10-076-622-122	Sequence 122, App	c 389	1.1	226	3	US-09-338-933-253	Sequence 253, App

C 390	19	1.1	226	3	US-09-338-933-254	Sequence 254, App	463	19	1.1	277	3	US-09-433-826B-101	Sequence 101, App
C 391	19	1.1	226	3	US-09-215-681-79	Sequence 79, App1	464	19	1.1	277	3	US-09-604-287A-101	Sequence 101, App
C 392	19	1.1	226	3	US-09-215-681-253	Sequence 253, App	465	19	1.1	277	3	US-09-285-480-101	Sequence 101, App
C 393	19	1.1	226	3	US-09-215-681-254	Sequence 254, App	466	19	1.1	277	3	US-09-834-759-101	Sequence 101, App
C 394	19	1.1	226	3	US-09-216-003A-79	Sequence 79, App1	467	19	1.1	277	3	US-09-590-751A-101	Sequence 101, App
C 395	19	1.1	226	3	US-09-216-003A-253	Sequence 253, App	468	19	1.1	277	3	US-09-551-621-101	Sequence 101, App
C 396	19	1.1	226	3	US-09-216-003A-254	Sequence 254, App	469	19	1.1	277	3	US-09-551-621A-101	Sequence 101, App
C 397	19	1.1	226	3	US-09-667-857-79	Sequence 79, App1	470	19	1.1	277	3	US-10-076-622-101	Sequence 101, App
C 398	19	1.1	226	3	US-09-667-857-253	Sequence 253, App	471	19	1.1	300	3	US-09-439-313-297	Sequence 297, App
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C 400	19	1.1	226	3	US-10-198-053-79	Sequence 79, App1	473	19	1.1	300	3	US-09-232-149A-297	Sequence 297, App
C 401	19	1.1	226	3	US-10-198-053-253	Sequence 253, App	474	19	1.1	300	3	US-09-159-812-297	Sequence 297, App
C 402	19	1.1	226	3	US-10-198-053-254	Sequence 254, App	475	19	1.1	300	3	US-09-636-215-297	Sequence 297, App
C 403	19	1.1	226	3	US-09-827-271-79	Sequence 79, App1	476	19	1.1	300	3	US-09-685-166A-297	Sequence 297, App
C 404	19	1.1	226	3	US-09-827-271-253	Sequence 253, App	477	19	1.1	300	3	US-09-688-489-297	Sequence 297, App
C 405	19	1.1	226	3	US-09-827-271-254	Sequence 254, App	478	19	1.1	300	3	US-09-679-426-297	Sequence 297, App
C 406	19	1.1	245	3	US-09-404-879A-305	Sequence 305, App	479	19	1.1	300	3	US-09-759-143-297	Sequence 297, App
C 407	19	1.1	245	3	US-09-338-933-305	Sequence 305, App	480	19	1.1	300	3	US-09-651-236-297	Sequence 297, App
C 408	19	1.1	245	3	US-09-215-681-305	Sequence 305, App	481	19	1.1	300	3	US-09-657-279-297	Sequence 297, App
C 409	19	1.1	245	3	US-09-216-003A-305	Sequence 305, App	482	19	1.1	300	3	US-10-012-896-297	Sequence 297, App
C 410	19	1.1	245	3	US-09-667-857-305	Sequence 305, App	C 483	19	1.1	307	3	US-09-404-879A-245	Sequence 245, App
C 411	19	1.1	245	3	US-10-198-053-305	Sequence 305, App	C 484	19	1.1	307	3	US-09-404-879A-299	Sequence 299, App
C 412	19	1.1	245	3	US-09-827-271-305	Sequence 305, App	C 485	19	1.1	307	3	US-09-338-933-245	Sequence 245, App
C 413	19	1.1	257	3	US-09-404-879A-207	Sequence 207, App	C 486	19	1.1	307	3	US-09-338-933-299	Sequence 299, App
C 414	19	1.1	257	3	US-09-404-879A-208	Sequence 208, App	C 487	19	1.1	307	3	US-09-215-681-299	Sequence 299, App
C 415	19	1.1	257	3	US-09-338-933-207	Sequence 207, App	C 488	19	1.1	307	3	US-09-215-681-245	Sequence 245, App
C 416	19	1.1	257	3	US-09-338-933-208	Sequence 208, App	C 489	19	1.1	307	3	US-09-216-003A-245	Sequence 245, App
C 417	19	1.1	257	3	US-09-215-681-207	Sequence 207, App	C 490	19	1.1	307	3	US-09-216-003A-299	Sequence 299, App
C 418	19	1.1	257	3	US-09-215-681-208	Sequence 208, App	C 491	19	1.1	307	3	US-09-667-857-245	Sequence 245, App
C 419	19	1.1	257	3	US-09-216-003A-207	Sequence 207, App	C 492	19	1.1	307	3	US-09-667-857-299	Sequence 299, App
C 420	19	1.1	257	3	US-09-216-003A-208	Sequence 208, App	C 493	19	1.1	307	3	US-10-198-053-245	Sequence 245, App
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C 422	19	1.1	257	3	US-09-667-857-208	Sequence 208, App	C 495	19	1.1	307	3	US-09-827-271-245	Sequence 245, App
C 423	19	1.1	257	3	US-10-198-053-207	Sequence 207, App	C 496	19	1.1	307	3	US-09-827-271-299	Sequence 299, App
C 424	19	1.1	257	3	US-10-198-053-208	Sequence 208, App	C 497	19	1.1	308	3	US-09-404-879A-289	Sequence 289, App
C 425	19	1.1	257	3	US-09-827-271-207	Sequence 207, App	C 498	19	1.1	308	3	US-09-338-933-289	Sequence 289, App
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C 427	19	1.1	260	3	US-09-404-879A-339	Sequence 339, App	C 500	19	1.1	308	3	US-09-216-003A-289	Sequence 289, App
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C 430	19	1.1	260	3	US-09-827-271-339	Sequence 339, App							
C 431	19	1.1	275	3	US-09-404-879A-227	Sequence 227, App							
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C 433	19	1.1	275	3	US-09-338-933-227	Sequence 227, App							
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C 456	19	1.1	276	3	US-10-198-053-169	Sequence 169, App							
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C 458	19	1.1	276	3	US-09-827-271-169	Sequence 169, App							
C 459	19	1.1	277	3	US-09-222-575-101	Sequence 101, App							
C 460	19	1.1	277	3	US-09-389-681-101	Sequence 101, App							
C 461	19	1.1	277	3	US-09-620-405B-101	Sequence 101, App							
C 462	19	1.1	277	3	US-09-339-338-101	Sequence 101, App							

RESULT 1

US-10-104-047-799

; Sequence 799, Application US/10104047

; Patent No. 6943241

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: No. 6943241el full length cdNA

; FILE REFERENCE: H1-A0105

; CURRENT APPLICATION NUMBER: US/10/104,047

; PRIOR FILING DATE: 2002-03-25

; PRIOR APPLICATION NUMBER:

; PRIOR FILING DATE:

; NUMBER OF SEQ ID NOS: 4096

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 799

; LENGTH: 1785

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-104-047-799

Query Match 93.1%; Score 1594; DB 3; Length 1785;

Best Local Similarity 99.9%; P: 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1694; Conservative

QY 1 ATGCCCGCCCTGGACACCCGCCCGCCAGCATCTGGGCTTCCACGCTTGGACCGTGGGAG 60

Db 90 ATGCCCGCCCTGGACACCCGCCCGCCAGCATCTGGGCTTCCACGCTTGGACCGTGGGAG 149

QY 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAACACCACTTCAGCCCCCAACGCCG 120

Db	150	CGGCCAACAGAGCTATGCTGGAGACATATGATAAACCACCTCAGCCCCACCAAGCCGC	209
Qy	121	CGCACCCGTTAGACAGACACCCCAAGAGACCTTGGGCCACCATGGGCGAGAGACATTACTTTC	180
Db	210	CGCACCCGTTAGACAGACACCCCAAGAGACCTTGGGCCACCATGGGCGAGAGACATTACTTTC	269
Qy	181	ATCTCTGGGCTCTGCTGAGCGGGCCCTTGGAGTCCGCCACCTGCTGCTCTGGCGACCC	240
Db	270	ATCTCTGGGCTCTGCTGAGCGGGCCCTTGGAGTCCGCCACCTGCTGCTCTGGCGACCC	329
Qy	241	TGGGTGTGGAGTGTGGTGGCGGCTGCTTCTGCTTCCGCGCGCTGCGGGGATTGCTTCCAG	300
Db	330	TGGGTGTGGAGTGTGGTGGCGGCTGCTTCTGCTTCCGCGCGCTGCGGGGATTGCTTCCAG	389
Qy	301	CGCTGTGGAGCTGTGTGGGGGATGACGCCCTTGTCTGTACTAGAGACTCACTGAG	360
Db	390	CGCTGTGGAGCTGTGTGGGGGATGACGCCCTTGTCTGTACTAGAGACTCACTGAG	449
Qy	361	GGGACTGCTGAAGCCAACTGGGCGCAAGGAGACAAATGGAGTGGCCCCCAGCCCTGATCGT	420
Db	450	GGGACTGCTGAAGCCAACTGGGCGCAAGGAGACAAATGGAGTGGCCCCCAGCCCTGATCGT	509
Qy	421	GCACCCCCCAGCGGGGATGGCCAGCGGCTCAAGTCAACCATGGGCGAGCAGCTTCAGC	480
Db	510	GCACCCCCCAGCGGGGATGGCCAGCGGCTCAAGTCAACCATGGGCGAGCAGCTTCAGC	569
Qy	481	TACCCCGATGTTAAGCTCAAGGCGATCCCTGTGTATCCCTTACCCGAGGGCCACCTCCCA	540
Db	570	TACCCCGATGTTAAGCTCAAGGCGATCCCTGTGTATCCCTTACCCGAGGGCCACCTCCCA	629
Qy	541	GCCCTGTAGCGGACTCTGCTGCAGGAGGCACTGGCCGATCCGCCATGCCAGTGCAGAC	600
Db	630	GCCCTGTAGCGGACTCTGCTGCAGGAGGCACTGGCCGATCCGCCATGCCAGTGCAGAC	689
Qy	601	AGCTGCCCCAGCACCTTTGGCAGTAGTCTCTGCTGGCTCCGAGGAGTACTATTCTTCCAT	660
Db	690	AGCTGCCCCAGCACCTTTGGCAGTAGTCTCTGCTGGCTCCGAGGAGTACTATTCTTCCAT	749
Qy	661	GAGTGGGACCTTGACCTGCGGAGATGGGAGTGGCTTCCATGTGAGCGCGAGAAATGTAT	720
Db	750	GAGTGGGACCTTGACCTGCGGAGATGGGAGTGGCTTCCATGTGAGCGCGAGAAATGTAT	809
Qy	721	GTGCTCATCTTCAAGAGCTGACAGAGCTGTTGAGGCTACACAGATCGATGAGCTGGCC	780
Db	810	GTGCTCATCTTCAAGAGCTGACAGAGCTGTTGAGGCTACACAGATCGATGAGCTGGCC	869
Qy	781	AAGTGACATCAGACACTGTGTTCTTGGAGAACACAGTAAGATCTCGGACCTTATCAGC	840
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Qy	841	AGCATCAGCAGGACTACCACTTGGATGAGCAGGATGCTGAGGGCCGCTGTGTAACGCGC	900
Db	930	AGCATCAGCAGGACTACCACTTGGATGAGCAGGATGCTGAGGGCCGCTGTGTAACGCGC	989
Qy	901	ATCATTTGCATTTAGTACCGGAAAGCGCTGCTGCGGCCACAGACCTCGGAGGCTCTTCA	960
Db	990	ATCATTTGCATTTAGTACCGGAAAGCGCTGCTGCGGCCACAGACCTCGGAGGCTCTTCA	1049
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Qy	1021	TCAGGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCAGGAGACGACTGCAGATGCC	1080
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Qy	1141	TTCCAGGGCACCGACACAGACTGCTCGGGGGACCCCTTCTCAGGTGACTGCTTAACCC	1200
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Qy	1381	TCCTTGATCCCGAGCTGGTCTGATCCCTGCGAGGGCCCTTCTCTCTCTCATGCTCT	1440
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Qy	1441	TCAGGTGGCTGTGATCATGGAAGTAAGGAGTTAGGCAATTAACCTTCTGGGAGTGAACCTG	1500
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Db	1770	CACAGTTTCTAAGTAC 1785	

RESULT 2

US-10-131-827-8473
; Sequence 8473, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8473
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(224)
; OTHER INFORMATION: n = A, C, T or G
US-10-131-827-8473

Query Match 1.5%; Score 25; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      189 GTAAGTACTCGCGCGGACCAACGC 213
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RESULT 3
US-10-131-827-8150
; Sequence 8150, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8150
; LENGTH: 170
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(170)
; OTHER INFORMATION: N = A, T, C or G
US-10-131-827-8150

Query Match      1.3%; Score 23; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      137 AAGTACTCGCGCGGACCAACGC 159
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RESULT 4
US-09-328-475C-111/C
; Sequence 111, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(468)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-111
```

```
Query Match      1.3%; Score 23; DB 3; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1691 AAGTACTCGCGCGGACCAACGC 1713
Db      104 AAGTACTCGCGCGGACCAACGC 82
|||||
RESULT 5
US-09-328-475C-246/C
; Sequence 246, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 246
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-328-475C-246

Query Match      1.3%; Score 23; DB 3; Length 482;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1691 AAGTACTCGCGCGGACCAACGC 1713
Db      104 AAGTACTCGCGCGGACCAACGC 82
|||||
RESULT 6
US-09-328-475C-239/C
; Sequence 239, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 239
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(483)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-239
```

```
Query Match      1.3%; Score 23; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCGCGCGGACCAACGC 1713
Db 104 AAGTACTCGCGCGGACCAACGC 82

RESULT 7
US-09-328-475C-224/c
; Sequence 224, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 224
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(494)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-224

Query Match      1.3%; Score 23; DB 3; Length 494;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCGCGCGGACCAACGC 1713
Db 103 AAGTACTCGCGCGGACCAACGC 81

RESULT 8
US-09-328-475C-185/c
; Sequence 185, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; TYPE: DNA
; ORGANISM: Homo Sapien

Query Match      1.3%; Score 23; DB 3; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCGCGCGGACCAACGC 1713
Db 100 AAGTACTCGCGCGGACCAACGC 78

RESULT 9
US-09-328-475C-181/c
; Sequence 181, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 181
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(501)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-181

Query Match      1.3%; Score 23; DB 3; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCGCGCGGACCAACGC 1713
Db 101 AAGTACTCGCGCGGACCAACGC 79

RESULT 10
US-09-328-475C-196/c
; Sequence 196, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 196
; TYPE: DNA
; ORGANISM: Homo Sapien
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/ SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 196
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(511)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-196

Query Match
Best Local Similarity 1.3%; Score 23; DB 3; Length 511;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGACCAACGC 1713
Db 106 AAGTACCTCGGCGGACCAACGC 84

RESULT 11
US-09-328-475C-305/c
; Sequence 305, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 305
; LENGTH: 719
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(719)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-305

Query Match
Best Local Similarity 1.3%; Score 23; DB 3; Length 719;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGACCAACGC 1713
Db 99 AAGTACCTCGGCGGACCAACGC 77

RESULT 12
US-09-328-475C-315/c
; Sequence 315, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
```

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/ TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 315
; LENGTH: 722
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(722)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-315

Query Match
Best Local Similarity 1.3%; Score 23; DB 3; Length 722;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGACCAACGC 1713
Db 95 AAGTACCTCGGCGGACCAACGC 73

RESULT 13
US-09-328-475C-277/c
; Sequence 277, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 277
; LENGTH: 724
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(724)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-277

Query Match
Best Local Similarity 1.3%; Score 23; DB 3; Length 724;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGACCAACGC 1713
Db 100 AAGTACCTCGGCGGACCAACGC 78

RESULT 14
US-09-328-475C-295
; Sequence 295, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
```

```
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 295
; LENGTH: 725
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(725)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-295

Query Match 1.3%; Score 23; DB 3; Length 725;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1691 AAGTACCTCGCGCGGACCGC 1713
Db 598 AAGTACCTCGCGCGGACCGC 620

RESULT 15
US-09-328-475C-329/c
; Sequence 329, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 329
; LENGTH: 725
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(725)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-329

Query Match 1.3%; Score 23; DB 3; Length 725;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1691 AAGTACCTCGCGCGGACCGC 1713
Db 97 AAGTACCTCGCGCGGACCGC 75

RESULT 16
US-09-328-475C-331/c
; Sequence 331, Application US/09328475C
; Patent No. 6476207
```

```
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 331
; LENGTH: 727
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(727)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-331

Query Match 1.3%; Score 23; DB 3; Length 727;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1691 AAGTACCTCGCGCGGACCGC 1713
Db 98 AAGTACCTCGCGCGGACCGC 76

RESULT 17
US-09-328-475C-294
; Sequence 294, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 294
; LENGTH: 736
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(736)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-294

Query Match 1.3%; Score 23; DB 3; Length 736;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1691 AAGTACCTCGCGCGGACCGC 1713
Db 619 AAGTACCTCGCGCGGACCGC 641
```

```
RESULT 18
US-09-328-475C-314/c
; Sequence 314, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 314
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(740)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-314

Query Match          1.3%; Score 23; DB 3; Length 740;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1691 AAGTACTCGGCGCGGACCACGC 1713
DB      123 AAGTACTCGGCGCGGACCACGC 101
|||||
|||||

RESULT 19
US-09-328-475C-304/c
; Sequence 304, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 304
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(741)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-304

Query Match          1.3%; Score 23; DB 3; Length 741;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1691 AAGTACTCGGCGCGGACCACGC 1713
DB      124 AAGTACTCGGCGCGGACCACGC 102
|||||
|||||

RESULT 20
US-09-328-475C-330/c
; Sequence 330, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(741)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-330

Query Match          1.3%; Score 23; DB 3; Length 741;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1691 AAGTACTCGGCGCGGACCACGC 1713
DB      122 AAGTACTCGGCGCGGACCACGC 100
|||||
|||||

RESULT 21
US-09-328-475C-276/c
; Sequence 276, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 276
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(744)
; OTHER INFORMATION: n = A,T,C or G
```


US-09-328-475C-276

Query Match 1.3%; Score 23; DB 3; Length 744;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCGCGCGGACACGC 1713
Db 123 AAGTACTCGCGCGGACACGC 101

RESULT 22

US-09-328-475C-328/c
; Sequence 328, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 328
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(747)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-328

Query Match 1.3%; Score 23; DB 3; Length 747;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCGCGCGGACACGC 1713
Db 122 AAGTACTCGCGCGGACACGC 100

RESULT 23

US-09-328-475C-158/c
; Sequence 158, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 772
; TYPE: DNA

; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(772)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-158

Query Match 1.3%; Score 23; DB 3; Length 772;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCGCGCGGACACGC 1713
Db 86 AAGTACTCGCGCGGACACGC 64

RESULT 24

US-09-328-475C-153/c
; Sequence 153, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 153
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(780)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-153

Query Match 1.3%; Score 23; DB 3; Length 780;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCGCGCGGACACGC 1713
Db 107 AAGTACTCGCGCGGACACGC 85

RESULT 25

US-09-280-116-268
; Sequence 268, Application US/09280116A
; Patent No. 631427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 268
; LENGTH: 781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: ubiquitin carboxyl-terminal hydrolases family 1

```
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(781)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-268

Query Match          1.3%; Score 23; DB 3; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGCGGACCAACGC 1713
Db 740 AAGTACCTCGGCGGCGGACCAACGC 762

RESULT 26
US-09-328-475C-167/c
; Sequence 167, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 167
; LENGTH: 797
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(797)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-167

Query Match          1.3%; Score 23; DB 3; Length 797;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGCGGACCAACGC 1713
Db 111 AAGTACCTCGGCGGCGGACCAACGC 89

RESULT 27
US-09-328-475C-229/c
; Sequence 229, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 229
; LENGTH: 815
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(815)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-229

Query Match          1.3%; Score 23; DB 3; Length 815;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGCGGACCAACGC 1713
Db 646 AAGTACCTCGGCGGCGGACCAACGC 668

RESULT 28
US-09-328-475C-240
; Sequence 240, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 240
; LENGTH: 815
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(815)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-240

Query Match          1.3%; Score 23; DB 3; Length 815;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGCGGACCAACGC 1713
Db 646 AAGTACCTCGGCGGCGGACCAACGC 668

RESULT 29
US-09-328-475C-249/c
; Sequence 249, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
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; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 249
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(821)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-249

Query Match          1.3%; Score 23; DB 3; Length 821;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCTGGCGCGGACACGCG 1713
Db 80 AAGTACTCTGGCGCGGACACGCG 58

RESULT 30
US-09-328-475C-245/c
; Sequence 245, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 245
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(822)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-245

Query Match          1.3%; Score 23; DB 3; Length 822;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCTGGCGCGGACACGCG 1713
Db 85 AAGTACTCTGGCGCGGACACGCG 63

RESULT 31
US-09-328-475C-191/c
; Sequence 191, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
```

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; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 191
; LENGTH: 823
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(823)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-191

Query Match          1.3%; Score 23; DB 3; Length 823;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCTGGCGCGGACACGCG 1713
Db 82 AAGTACTCTGGCGCGGACACGCG 60

RESULT 32
US-09-328-475C-255/c
; Sequence 255, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 255
; LENGTH: 830
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(830)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-255

Query Match          1.3%; Score 23; DB 3; Length 830;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCTGGCGCGGACACGCG 1713
Db 113 AAGTACTCTGGCGCGGACACGCG 91

RESULT 33
US-09-328-475C-43/c
; Sequence 43, Application US/09328475C
; Patent No. 6476207
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; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1020)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-43

Query Match          1.3%; Score 23; DB 3; Length 1020;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGACCAACGC 1713
    |||||||
Db 100 AAGTACCTCGGCGGACCAACGC 78

RESULT 34
US-09-328-475C-102
; Sequence 102, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1020)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-102

Query Match          1.3%; Score 23; DB 3; Length 1020;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGACCAACGC 1713
    |||||||
Db 526 AAGTACCTCGGCGGACCAACGC 548
```

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RESULT 35
US-09-328-475C-103/c
; Sequence 103, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 103
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1021)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-103

Query Match          1.3%; Score 23; DB 3; Length 1021;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGACCAACGC 1713
    |||||||
Db 101 AAGTACCTCGGCGGACCAACGC 79

RESULT 36
US-09-328-475C-51/c
; Sequence 51, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-51

Query Match          1.3%; Score 23; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 99 AAGTACCTCGCGCGGACCAACGC 77

RESULT 37
US-09-328-475C-56/c
; Sequence 56, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-56

Query Match 1.3%; Score 23; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 111 AAGTACCTCGCGCGGACCAACGC 89

RESULT 38
US-09-328-475C-71/c
; Sequence 71, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-71
```

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US-09-328-475C-71

Query Match 1.3%; Score 23; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 100 AAGTACCTCGCGCGGACCAACGC 78

RESULT 39
US-09-328-475C-77/c
; Sequence 77, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-77

Query Match 1.3%; Score 23; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 106 AAGTACCTCGCGCGGACCAACGC 84

RESULT 40
US-09-328-475C-78
; Sequence 78, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 78
; LENGTH: 1024
; TYPE: DNA
US-09-328-475C-78
```

```
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-78
```

```
Query Match 1.3%; Score 23; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1691 AAGTACTCGCGCGGACCAACGC 1713
Db 515 AAGTACTCGCGCGGACCAACGC 537
```

```
RESULT 41
US-09-328-475C-93/c
; Sequence 93, Application US/09328475C
; Patent No. 6476207
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532,002/200130,463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
```

```
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 93
; LENGTH: 1024
```

```
; TYPE: DNA
```

```
; ORGANISM: Homo Sapien
```

```
; FEATURE:
```

```
; NAME/KEY: misc feature
```

```
; LOCATION: (1)...(1024)
```

```
; OTHER INFORMATION: n = A,T,C or G
```

```
US-09-328-475C-93
```

```
Query Match 1.3%; Score 23; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1691 AAGTACTCGCGCGGACCAACGC 1713
Db 100 AAGTACTCGCGCGGACCAACGC 78
```

```
RESULT 42
US-09-328-475C-334
; Sequence 334, Application US/09328475C
; Patent No. 6476207
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
```

```
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532,002/200130,463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
```

```
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 334
; LENGTH: 2051
```

```
; TYPE: DNA
```

```
; ORGANISM: Homo sapien
```

```
; FEATURE:
```

```
; NAME/KEY: misc feature
```

```
; LOCATION: (1)...(2051)
```

```
; OTHER INFORMATION: n = A,T,C or G
```

```
US-09-328-475C-334
```

```
Query Match 1.3%; Score 23; DB 3; Length 2051;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1691 AAGTACTCGCGCGGACCAACGC 1713
Db 1814 AAGTACTCGCGCGGACCAACGC 1836
```

```
RESULT 43
```

```
US-09-902-540-8302
```

```
; Sequence 8302, Application US/09902540
```

```
; Patent No. 6833447
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Goldman, Barry S.
```

```
; APPLICANT: Hinkle, Gregory J.
```

```
; APPLICANT: Slater, Steven C.
```

```
; APPLICANT: Wiegand, Roger C.
```

```
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
```

```
; FILE REFERENCE: 38-10(15849)B
```

```
; CURRENT APPLICATION NUMBER: US/09/902,540
```

```
; CURRENT FILING DATE: 2001-07-10
```

```
; PRIOR APPLICATION NUMBER: 60/217,883
```

```
; PRIOR FILING DATE: 2000-07-10
```

```
; NUMBER OF SEQ ID NOS: 16825
```

```
; SEQ ID NO 8302
```

```
; LENGTH: 2253
```

```
; TYPE: DNA
```

```
; ORGANISM: Myxococcus xanthus
```

```
US-09-902-540-8302
```

```
Query Match 1.3%; Score 23; DB 3; Length 2253;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 666 GGACCTGGACCTGCGCGAGATGG 688
Db 1188 GGACCTGGACCTGCGCGAGATGG 1210
```

```
RESULT 44
```

```
US-09-902-540-866
```

```
; Sequence 866, Application US/09902540
```

```
; Patent No. 6833447
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Goldman, Barry S.
```

```
; APPLICANT: Hinkle, Gregory J.
```

```
; APPLICANT: Slater, Steven C.
```

```
; APPLICANT: Wiegand, Roger C.
```

```
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
```

```
; FILE REFERENCE: 38-10(15849)B
```

```
; CURRENT APPLICATION NUMBER: US/09/902,540
```

```
; CURRENT FILING DATE: 2001-07-10
```

```
; PRIOR APPLICATION NUMBER: 60/217,883
```

```
; PRIOR FILING DATE: 2000-07-10
```

```
; NUMBER OF SEQ ID NOS: 16825
```

```
; SEQ ID NO 866
```

```
; LENGTH: 6339
```

```
; TYPE: DNA
```

```
; ORGANISM: Myxococcus xanthus
```

```
US-09-902-540-866
```

Query Match 1.3%; Score 23; DB 3; Length 6339;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 666 GGACCTGGACTGCGCGAGATGG 688
DB 1190 GGACCTGGACTGCGCGAGATGG 1212

RESULT 45

US-09-188-930-4/c

; Sequence 4, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 311
; TYPE: DNA
; ORGANISM: Human
US-09-188-930-4

Query Match 1.3%; Score 22; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGACCCAGCG 1713
DB 23 AGTACTCGCGCGACCCAGCG 2

RESULT 46

US-09-312-283C-4/c

; Sequence 4, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 311
; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283C-4

Query Match 1.3%; Score 22; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGACCCAGCG 1713
DB 23 AGTACTCGCGCGACCCAGCG 2

RESULT 47

US-10-002-344A-138
; Sequence 138, Application US/10002344A
; Patent No. 6846650
; GENERAL INFORMATION:
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yongming
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Proteins
; FILE REFERENCE: DEX-0241
; CURRENT APPLICATION NUMBER: US/10/002,344A
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/242,998
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-002-344A-138

Query Match 1.3%; Score 22; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGACCCAGCG 1713
DB 326 AGTACTCGCGCGACCCAGCG 347

RESULT 48

US-09-328-475C-237/c
; Sequence 237, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroil III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 237
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(483)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-237

Query Match 1.3%; Score 22; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGACCCAGCG 1713
DB 103 AGTACTCGCGCGACCCAGCG 82


```
RESULT 49
US-09-328-475C-222/c
; Sequence 222, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 222
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-328-475C-222

Query Match          1.3%; Score 22; DB 3; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
DB 103 AGTACTCGCGCGGACACGC 82

RESULT 50
US-09-328-475C-194
; Sequence 194, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 194
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-328-475C-194

Query Match          1.3%; Score 22; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
DB 309 AGTACTCGCGCGGACACGC 330

RESULT 51
US-09-328-475C-200/c
```

```
; Sequence 200, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 200
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(506)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-200

Query Match          1.3%; Score 22; DB 3; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
DB 104 AGTACTCGCGCGGACACGC 83

RESULT 52
US-10-131-827-8248
; Sequence 8248, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8248
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-8248

Query Match          1.3%; Score 22; DB 3; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
DB 568 AGTACTCGCGCGGACACGC 589

RESULT 53
```

US-09-328-475C-281/c
; Sequence 281, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 281
; LENGTH: 727
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(727)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-281

Query Match 1.3%; Score 22; DB 3; Length 727;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGACACGCG 1713
DB 97 AGTACTCTGGCGCGACACGCG 76

RESULT 54
US-09-328-475C-280/c
; Sequence 280, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 280
; LENGTH: 751
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(751)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-280

Query Match 1.3%; Score 22; DB 3; Length 751;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGACACGCG 1713

DB 122 AGTACTCTGGCGCGACACGCG 101
RESULT 55
US-09-328-475C-169
; Sequence 169, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 169
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(771)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-169

Query Match 1.3%; Score 22; DB 3; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGACACGCG 1713
DB 291 AGTACTCTGGCGCGACACGCG 312

RESULT 56
US-09-328-475C-176/c
; Sequence 176, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(773)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-176

```
Query Match          1.3%; Score 22; DB 3; Length 773;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGGACACGCG 1713
DB 86 AGTACTCTGGCGCGGACACGCG 65

RESULT 57
US-09-328-475C-163/c
; Sequence 163, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 776
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(776)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-163

Query Match          1.3%; Score 22; DB 3; Length 776;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGGACACGCG 1713
DB 101 AGTACTCTGGCGCGGACACGCG 80

RESULT 58
US-09-328-475C-168/c
; Sequence 168, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 168
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(780)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-168

Query Match          1.3%; Score 22; DB 3; Length 780;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGGACACGCG 1713
DB 102 AGTACTCTGGCGCGGACACGCG 81

RESULT 59
US-09-328-475C-119/c
; Sequence 119, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 119
; LENGTH: 811
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(811)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-119

Query Match          1.3%; Score 22; DB 3; Length 811;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGGACACGCG 1713
DB 81 AGTACTCTGGCGCGGACACGCG 60

RESULT 60
US-09-328-475C-238
; Sequence 238, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
```

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; SEQ ID NO 238
; LENGTH: 815
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(815)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-238

Query Match      1.3%; Score 22; DB 3; Length 815;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1692 AGTACCTCGCGCGGACCAACGC 1713
Db      496 AGTACCTCGCGCGGACCAACGC 517

RESULT 61
US-09-328-475C-223
; Sequence 223, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 223
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(822)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-223

Query Match      1.3%; Score 22; DB 3; Length 822;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1692 AGTACCTCGCGCGGACCAACGC 1713
Db      506 AGTACCTCGCGCGGACCAACGC 527

RESULT 62
US-09-328-475C-195/c
; Sequence 195, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
```

```
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 195
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(848)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-195

Query Match      1.3%; Score 22; DB 3; Length 848;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1692 AGTACCTCGCGCGGACCAACGC 1713
Db      99 AGTACCTCGCGCGGACCAACGC 78

RESULT 63
US-09-328-475C-104/c
; Sequence 104, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1017)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-104

Query Match      1.3%; Score 22; DB 3; Length 1017;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1692 AGTACCTCGCGCGGACCAACGC 1713
Db      101 AGTACCTCGCGCGGACCAACGC 80

RESULT 64
US-09-328-475C-57/c
; Sequence 57, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
```

```
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-57

Query Match          1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGGACCCACGC 1713
Db 103 AGTACTCTGGCGCGGACCCACGC 82

RESULT 65
US-09-328-475C-61
; Sequence 61, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-61

Query Match          1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGGACCCACGC 1713
Db 665 AGTACTCTGGCGCGGACCCACGC 686

RESULT 66
US-09-328-475C-62/c
; Sequence 62, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
```

```
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-62

Query Match          1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGGACCCACGC 1713
Db 104 AGTACTCTGGCGCGGACCCACGC 83

RESULT 67
US-09-328-475C-65/c
; Sequence 65, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-65

Query Match          1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGGACCCACGC 1713
Db 103 AGTACTCTGGCGCGGACCCACGC 82
```

```
RESULT 68
US-09-328-475C-73/c
; Sequence 73, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-73

Query Match          1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACCTCGCGCGGACCGC 1713
DB 105 AGTACCTCGCGCGGACCGC 84

RESULT 69
US-09-328-475C-75/c
; Sequence 75, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-75

Query Match          1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-328-475C-79
; Sequence 79, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-79

Query Match          1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACCTCGCGCGGACCGC 1713
DB 399 AGTACCTCGCGCGGACCGC 420

RESULT 70
US-09-328-475C-79
; Sequence 79, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-79

Query Match          1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACCTCGCGCGGACCGC 1713
DB 399 AGTACCTCGCGCGGACCGC 420

RESULT 71
US-09-328-475C-80/c
; Sequence 80, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-80

Query Match          1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Query Match      1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
Db 110 AGTACTCGCGCGGACACGC 89

RESULT 72
US-09-328-475C-82/c
; Sequence 82, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-82

Query Match      1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
Db 104 AGTACTCGCGCGGACACGC 83

RESULT 73
US-09-328-475C-86/c
; Sequence 86, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
```

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-86

Query Match      1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
Db 111 AGTACTCGCGCGGACACGC 90

RESULT 74
US-09-188-930-249/c
; Sequence 249, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 249
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Human
US-09-188-930-249

Query Match      1.3%; Score 22; DB 3; Length 1212;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
Db 24 AGTACTCGCGCGGACACGC 3

RESULT 75
US-09-312-283C-249/c
; Sequence 249, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283C-249

Query Match      1.3%; Score 22; DB 3; Length 1212;
Best Local Similarity 100.0%; Pred. No. 1.9;
```



```
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1692 AGTACTCGCGCGGACACGC 1713
Db 24 AGTACTCGCGCGGACACGC 3
|||||
RESULT 76
US-10-131-827-8652
; Sequence 8652, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8652
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-8652
Query Match 1.2%; Score 21; DB 3; Length 159;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1693 GTACCTCGCGCGGACACGC 1713
Db 128 GTACCTCGCGCGGACACGC 148
|||||
RESULT 77
US-10-131-827-8632
; Sequence 8632, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8632
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-8632
Query Match 1.2%; Score 21; DB 3; Length 240;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1693 GTACCTCGCGCGGACACGC 1713
|||||
```

```
Db 209 GTACCTCGCGCGGACACGC 229
|||||
RESULT 78
US-09-389-681-319
; Sequence 319, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.47003
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-389-681-319
Query Match 1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1693 GTACCTCGCGCGGACACGC 1713
Db 208 GTACCTCGCGCGGACACGC 228
|||||
RESULT 79
US-09-620-405B-319
; Sequence 319, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.47008
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-620-405B-319
Query Match 1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1693 GTACCTCGCGCGGACACGC 1713
|||||
```

```
Db      208 GTACCTCGGCGCGACCAAGC 228

RESULT 80
US-09-433-826B-319
; Sequence 319, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-433-826B-319

Query Match      1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1693 GTACCTCGGCGCGACCAAGC 1713
|||||
Db      208 GTACCTCGGCGCGACCAAGC 228

RESULT 81
US-09-604-287A-319
; Sequence 319, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-604-287A-319

Query Match      1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1693 GTACCTCGGCGCGACCAAGC 1713
|||||

Db      208 GTACCTCGGCGCGACCAAGC 228

RESULT 82
US-09-834-759-319
; Sequence 319, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-759-319

Query Match      1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1693 GTACCTCGGCGCGACCAAGC 1713
|||||
Db      208 GTACCTCGGCGCGACCAAGC 228

RESULT 83
US-09-590-751A-319
; Sequence 319, Application US/09590751A
; Patent No. 6756477
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C6
; CURRENT APPLICATION NUMBER: US/09/590,751A
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-590-751A-319

Query Match      1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1693 GTACCTCGGCGCGACCAAGC 1713
|||||
```

Db 208 GTACCTCGCGCGGACCACGC 228
|||||
RESULT 84
US-09-551-621-319
; Sequence 319, Application US/09551621
; Patent No. 6825175
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C5
; CURRENT FILING DATE: 2000-04-17
; CURRENT APPLICATION NUMBER: US/09/551,621
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-551-621-319
Query Match 1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1693 GTACCTCGCGCGGACCACGC 1713
|||||
Db 208 GTACCTCGCGCGGACCACGC 228
RESULT 85
US-09-551-621A-319
; Sequence 319, Application US/09551621A
; Patent No. 6844325
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C5
; CURRENT FILING DATE: 2000-04-17
; CURRENT APPLICATION NUMBER: US/09/551,621A
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-551-621A-319
Query Match 1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1693 GTACCTCGCGCGGACCACGC 1713
|||||

Db 208 GTACCTCGCGCGGACCACGC 228
RESULT 86
US-10-076-622-319
; Sequence 319, Application US/10076622
; Patent No. 6958361
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C11
; CURRENT FILING DATE: 2002-02-13
; CURRENT APPLICATION NUMBER: US/10/076,622
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 24, 36, 39
; OTHER INFORMATION: n = A,T,C or G
US-10-076-622-319
Query Match 1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1693 GTACCTCGCGCGGACCACGC 1713
|||||
Db 208 GTACCTCGCGCGGACCACGC 228
RESULT 87
US-09-439-313-293
; Sequence 293, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT FILING DATE: 1999-11-12
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-293
Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1693 GTACCTCGCGCGGACCACGC 1713
|||||
Db 232 GTACCTCGCGCGGACCACGC 252
|||||

```
RESULT 88
US-09-352-616A-293
; Sequence 293, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-293
Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGGCGGACACGC 1713
Db 232 GTACCTCGGCGGACACGC 252

RESULT 89
US-09-232-149A-293
; Sequence 293, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-293
Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGGCGGACACGC 1713
Db 232 GTACCTCGGCGGACACGC 252

RESULT 90
US-09-159-812-293
; Sequence 293, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
```

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; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-159-812-293
Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGGCGGACACGC 1713
Db 232 GTACCTCGGCGGACACGC 252

RESULT 91
US-09-636-215-293
; Sequence 293, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-293
Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGGCGGACACGC 1713
Db 232 GTACCTCGGCGGACACGC 252

RESULT 92
US-09-685-166A-293
; Sequence 293, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
```

; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685.166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166A-293

Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGCGCGGACACGC 1713
|||||
Db 232 GTACCTCGCGCGGACACGC 252

RESULT 93
US-09-688-489-293
; Sequence 293, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688.489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-688-489-293

Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGCGCGGACACGC 1713
|||||
Db 232 GTACCTCGCGCGGACACGC 252

RESULT 94
US-09-679-426-293
; Sequence 293, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679.426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-679-426-293

Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGCGCGGACACGC 1713
|||||
Db 232 GTACCTCGCGCGGACACGC 252

RESULT 95
US-09-759-143-293
; Sequence 293, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759.143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-293

Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 232 GTACCTCGGCGGACCGC 252

RESULT 96

US-09-651-236-293

; Sequence 293, Application US/09651236

; Patent No. 6818751

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.42718C18

; CURRENT APPLICATION NUMBER: US/09/651,236

; CURRENT FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 865

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 293

; LENGTH: 301

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-651-236-293

Query Match

Best Local Similarity 1.2%; Score 21; DB 3; Length 301;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 97

US-09-657-279-293

; Sequence 293, Application US/09657279

; Patent No. 6894146

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C19

; CURRENT APPLICATION NUMBER: US/09/657,279

; CURRENT FILING DATE: 2000-09-06

; NUMBER OF SEQ ID NOS: 877

; SOFTWARE: FastSeq for Windows Version 3.0

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; ORGANISM: Homo sapien

US-09-657-279-293

Query Match

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US-10-012-896-293

; Sequence 293, Application US/10012896

; Patent No. 6943236

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals de Bassols, Carlota

; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.

; APPLICANT: Wantanabe, Yoshihiro

; APPLICANT: Meagher, Madeleine Joy

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C27

; CURRENT APPLICATION NUMBER: US/10/012,896

; CURRENT FILING DATE: 2001-12-10

; NUMBER OF SEQ ID NOS: 1011

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 293

; LENGTH: 301

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-012-896-293

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; Sequence 8546, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-8546

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; Sequence 71, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
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; TYPE: DNA
; ORGANISM: Human
US-09-188-930-71

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Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 329 secs

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	C 115	24	1.4	894	5	US-10-198-846-5595	Sequence 5595, Ap	C 188	23	1.3	178	3	US-09-814-353-6340	Sequence 6340, Ap
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	C 133	23	1.3	111	3	US-09-732-560-42	Sequence 42, Appl	C 206	23	1.3	189	3	US-09-814-353-16163	Sequence 16163, A
	C 134	23	1.3	114	8	US-10-357-930-37310	Sequence 37310, A	C 207	23	1.3	190	3	US-09-814-353-3622	Sequence 3622, Ap
	C 135	23	1.3	117	9	US-10-950-009-845	Sequence 845, App	C 208	23	1.3	190	3	US-09-814-353-9936	Sequence 9936, Ap
	C 136	23	1.3	119	3	US-09-732-560-45	Sequence 45, Appl	C 209	23	1.3	190	8	US-10-357-930-37701	Sequence 37701, A
	C 137	23	1.3	122	6	US-10-125-968-1322	Sequence 1322, Ap	C 210	23	1.3	191	3	US-09-814-353-18492	Sequence 18492, A
	C 138	23	1.3	127	3	US-09-814-353-6064	Sequence 6064, Ap	C 211	23	1.3	191	8	US-10-357-930-7331	Sequence 7331, Ap
	C 139	23	1.3	127	3	US-09-814-353-12343	Sequence 12343, A	C 212	23	1.3	193	8	US-10-357-930-37634	Sequence 37634, A
	C 140	23	1.3	128	3	US-09-814-353-5052	Sequence 5052, Ap	C 213	23	1.3	195	3	US-09-814-353-5805	Sequence 5805, Ap
	C 141	23	1.3	128	3	US-09-814-353-11344	Sequence 11344, A	C 214	23	1.3	195	3	US-09-814-353-12088	Sequence 12088, A
	C 142	23	1.3	133	3	US-09-814-353-5393	Sequence 5393, Ap	C 215	23	1.3	195	3	US-09-814-353-18727	Sequence 18727, A
	C 143	23	1.3	133	3	US-09-814-353-11680	Sequence 11680, A	C 216	23	1.3	195	8	US-10-357-930-37485	Sequence 37485, A
	C 144	23	1.3	136	8	US-10-357-930-7452	Sequence 7452, Ap	C 217	23	1.3	196	8	US-10-357-930-36921	Sequence 36921, A
	C 145	23	1.3	140	3	US-09-814-353-17414	Sequence 17414, A	C 218	23	1.3	196	8	US-10-357-930-38099	Sequence 38099, A
	C 146	23	1.3	142	3	US-09-814-353-4669	Sequence 4669, Ap	C 219	23	1.3	198	3	US-09-732-560-26	Sequence 26, Appl
	C 147	23	1.3	142	3	US-09-814-353-10968	Sequence 10968, A	C 220	23	1.3	198	3	US-09-814-353-4802	Sequence 4802, Ap
	C 148	23	1.3	142	8	US-10-357-930-37807	Sequence 37807, A	C 221	23	1.3	198	3	US-09-814-353-11099	Sequence 11099, A
	C 149	23	1.3	143	3	US-09-814-353-18749	Sequence 18749, A	C 222	23	1.3	200	3	US-09-814-353-6265	Sequence 6265, Ap
	C 150	23	1.3	147	3	US-09-814-353-5092	Sequence 5092, Ap	C 223	23	1.3	200	3	US-09-814-353-12543	Sequence 12543, A
	C 151	23	1.3	147	9	US-10-950-009-514	Sequence 514, App	C 224	23	1.3	200	8	US-10-357-930-8126	Sequence 8126, Ap
	C 152	23	1.3	147	3	US-09-814-353-11384	Sequence 11384, A	C 225	23	1.3	203	3	US-09-814-353-5532	Sequence 5532, Ap
	C 153	23	1.3	149	3	US-09-814-353-5529	Sequence 5529, Ap	C 226	23	1.3	203	3	US-09-814-353-11819	Sequence 11819, A
	C 154	23	1.3	149	3	US-09-814-353-11816	Sequence 11816, A	C 227	23	1.3	203	3	US-09-814-353-18739	Sequence 18739, A
	C 155	23	1.3	149	8	US-10-357-930-7423	Sequence 7423, Ap	C 228	23	1.3	203	3	US-09-814-353-18771	Sequence 18771, A
	C 156	23	1.3	150	3	US-09-814-353-17146	Sequence 17146, A	C 229	23	1.3	205	3	US-09-814-353-18249	Sequence 18249, A
	C 157	23	1.3	150	8	US-10-357-930-37363	Sequence 37363, A	C 230	23	1.3	206	3	US-09-814-353-18427	Sequence 18427, A
	C 158	23	1.3	151	3	US-09-814-353-6037	Sequence 6037, Ap	C 231	23	1.3	207	3	US-09-732-560-48	Sequence 48, Appl
	C 159	23	1.3	151	3	US-09-814-353-12316	Sequence 12316, A	C 232	23	1.3	207	8	US-10-357-930-7941	Sequence 7941, Ap
	C 160	23	1.3	153	3	US-09-732-560-86	Sequence 86, Appl	C 233	23	1.3	209	3	US-09-814-353-3605	Sequence 3605, Ap
	C 161	23	1.3	156	3	US-09-814-353-11307	Sequence 11307, A	C 234	23	1.3	209	3	US-09-814-353-6271	Sequence 6271, Ap
	C 162	23	1.3	156	3	US-09-814-353-5015	Sequence 5015, Ap	C 235	23	1.3	209	3	US-09-814-353-9919	Sequence 9919, Ap
	C 163	23	1.3	157	9	US-10-950-009-622	Sequence 622, App	C 236	23	1.3	209	8	US-09-814-353-12549	Sequence 12549, A
	C 164	23	1.3	160	3	US-09-732-560-113	Sequence 113, App	C 237	23	1.3	209	8	US-10-357-930-7946	Sequence 7946, Ap
	C 165	23	1.3	167	8	US-10-357-930-6085	Sequence 6085, Ap	C 238	23	1.3	210	3	US-09-814-353-18700	Sequence 18700, A
	C 166	23	1.3	167	8	US-10-357-930-37715	Sequence 37715, A	C 239	23	1.3	211	8	US-10-357-930-8217	Sequence 8217, Ap
	C 167	23	1.3	168	3	US-09-814-353-4256	Sequence 4256, Ap	C 240	23	1.3	211	8	US-10-357-930-37414	Sequence 37414, A
	C 168	23	1.3	168	3	US-09-814-353-10560	Sequence 10560, A	C 241	23	1.3	212	6	US-10-125-968-1417	Sequence 1417, Ap
	C 169	23	1.3	169	8	US-10-357-930-37554	Sequence 37554, A	C 242	23	1.3	212	9	US-10-950-009-958	Sequence 958, App

C 243	23	1.3	213	3	US-09-814-353-18481	Sequence 18481, A	C 316	23	1.3	266	8	US-10-357-930-45119	Sequence 45119, A
C 244	23	1.3	214	8	US-10-357-930-38041	Sequence 38041, A	C 317	23	1.3	267	8	US-10-357-930-37696	Sequence 37696, A
C 245	23	1.3	217	8	US-10-357-930-7368	Sequence 7368, A	C 318	23	1.3	267	8	US-10-357-930-37772	Sequence 37772, A
C 246	23	1.3	220	8	US-10-357-930-7328	Sequence 7328, A	C 319	23	1.3	268	3	US-09-814-353-6031	Sequence 6031, A
C 247	23	1.3	221	3	US-09-814-353-18201	Sequence 18201, A	C 320	23	1.3	268	3	US-09-814-353-12310	Sequence 12310, A
C 248	23	1.3	222	3	US-09-814-353-17728	Sequence 17728, A	C 321	23	1.3	268	8	US-10-357-930-38743	Sequence 38743, A
C 249	23	1.3	222	3	US-09-814-353-18350	Sequence 18350, A	C 322	23	1.3	269	8	US-10-357-930-8009	Sequence 8009, A
C 250	23	1.3	226	3	US-09-814-353-5530	Sequence 5530, A	C 323	23	1.3	271	3	US-09-814-353-4954	Sequence 4954, A
C 251	23	1.3	226	3	US-09-814-353-11817	Sequence 11817, A	C 324	23	1.3	271	3	US-09-814-353-11247	Sequence 11247, A
C 252	23	1.3	227	3	US-09-814-353-6041	Sequence 6041, A	C 325	23	1.3	271	3	US-09-814-353-16944	Sequence 16944, A
C 253	23	1.3	227	3	US-09-814-353-12320	Sequence 12320, A	C 326	23	1.3	272	3	US-09-814-353-5153	Sequence 5153, A
C 254	23	1.3	227	6	US-10-125-968-1238	Sequence 1238, A	C 327	23	1.3	272	3	US-09-814-353-5377	Sequence 5377, A
C 255	23	1.3	227	8	US-10-357-930-7987	Sequence 7987, A	C 328	23	1.3	272	3	US-09-814-353-11444	Sequence 11444, A
C 256	23	1.3	231	3	US-09-814-353-18092	Sequence 18092, A	C 329	23	1.3	272	3	US-09-814-353-11664	Sequence 11664, A
C 257	23	1.3	234	3	US-09-814-353-17216	Sequence 17216, A	C 330	23	1.3	273	3	US-09-814-353-5232	Sequence 5232, A
C 258	23	1.3	234	8	US-10-357-930-37410	Sequence 37410, A	C 331	23	1.3	273	3	US-09-814-353-11519	Sequence 11519, A
C 259	23	1.3	235	3	US-09-814-353-4764	Sequence 4764, A	C 332	23	1.3	273	5	US-10-060-036-4354	Sequence 4354, A
C 260	23	1.3	235	3	US-09-814-353-5885	Sequence 5885, A	C 333	23	1.3	276	3	US-09-732-560-40	Sequence 40, Appl
C 261	23	1.3	235	3	US-09-814-353-11061	Sequence 11061, A	C 334	23	1.3	277	8	US-10-357-930-37632	Sequence 37632, A
C 262	23	1.3	235	3	US-09-814-353-12166	Sequence 12166, A	C 335	23	1.3	277	8	US-10-357-930-37955	Sequence 37955, A
C 263	23	1.3	235	8	US-10-357-930-7559	Sequence 7559, A	C 336	23	1.3	277	9	US-10-950-009-158	Sequence 158, Appl
C 264	23	1.3	236	6	US-10-125-968-1262	Sequence 1262, A	C 337	23	1.3	278	3	US-09-969-034-22	Sequence 22, Appl
C 265	23	1.3	237	8	US-10-357-930-7525	Sequence 7525, A	C 338	23	1.3	279	3	US-09-814-353-6306	Sequence 6306, A
C 266	23	1.3	238	3	US-09-732-560-74	Sequence 74, Appl	C 339	23	1.3	279	3	US-09-814-353-12584	Sequence 12584, A
C 267	23	1.3	241	8	US-10-357-930-7977	Sequence 7977, A	C 340	23	1.3	279	3	US-09-814-353-17446	Sequence 17446, A
C 268	23	1.3	241	8	US-10-357-930-8241	Sequence 8241, A	C 341	23	1.3	279	8	US-10-357-930-7448	Sequence 7448, A
C 269	23	1.3	241	9	US-10-950-009-221	Sequence 221, Appl	C 342	23	1.3	280	7	US-10-663-561-165	Sequence 165, Appl
C 270	23	1.3	244	8	US-10-357-930-7837	Sequence 7837, A	C 343	23	1.3	281	8	US-10-357-930-35994	Sequence 35994, A
C 271	23	1.3	244	8	US-10-066-543-41	Sequence 41, Appl	C 344	23	1.3	282	3	US-09-814-353-4714	Sequence 4714, A
C 272	23	1.3	245	5	US-10-066-543-41	Sequence 41, Appl	C 345	23	1.3	282	3	US-09-814-353-5711	Sequence 5711, A
C 273	23	1.3	246	3	US-09-814-353-5423	Sequence 5423, A	C 346	23	1.3	282	3	US-09-814-353-11012	Sequence 11012, A
C 274	23	1.3	247	3	US-09-814-353-11710	Sequence 11710, A	C 347	23	1.3	282	3	US-09-814-353-11995	Sequence 11995, A
C 275	23	1.3	247	9	US-09-814-353-18754	Sequence 18754, A	C 348	23	1.3	282	8	US-10-357-930-8051	Sequence 8051, A
C 276	23	1.3	248	3	US-09-814-353-5058	Sequence 5058, A	C 349	23	1.3	283	3	US-09-814-353-2079	Sequence 2079, A
C 277	23	1.3	248	3	US-09-814-353-11350	Sequence 11350, A	C 350	23	1.3	283	3	US-09-814-353-8423	Sequence 8423, A
C 278	23	1.3	248	3	US-09-814-353-17941	Sequence 17941, A	C 351	23	1.3	283	3	US-09-814-353-17932	Sequence 17932, A
C 279	23	1.3	249	3	US-09-814-353-5845	Sequence 5845, A	C 352	23	1.3	284	6	US-10-125-968-1124	Sequence 1124, A
C 280	23	1.3	249	3	US-09-814-353-12097	Sequence 12097, A	C 353	23	1.3	284	6	US-10-125-968-1124	Sequence 1124, A
C 281	23	1.3	250	3	US-09-814-353-3331	Sequence 3331, A	C 354	23	1.3	285	8	US-10-723-860-1154	Sequence 1154, A
C 282	23	1.3	250	3	US-09-814-353-9652	Sequence 9652, A	C 355	23	1.3	285	8	US-10-357-930-37293	Sequence 37293, A
C 283	23	1.3	250	9	US-10-950-009-672	Sequence 672, Appl	C 356	23	1.3	285	9	US-10-950-009-824	Sequence 824, Appl
C 284	23	1.3	252	8	US-10-357-930-38132	Sequence 38132, A	C 357	23	1.3	285	9	US-10-756-149-1120	Sequence 1120, A
C 285	23	1.3	253	3	US-09-814-353-4885	Sequence 4885, A	C 358	23	1.3	287	3	US-09-814-353-5598	Sequence 5598, A
C 286	23	1.3	253	3	US-09-814-353-5270	Sequence 5270, A	C 359	23	1.3	287	3	US-09-814-353-6310	Sequence 6310, A
C 287	23	1.3	253	3	US-09-814-353-11181	Sequence 11181, A	C 360	23	1.3	287	3	US-09-814-353-11885	Sequence 11885, A
C 288	23	1.3	253	3	US-09-814-353-11557	Sequence 11557, A	C 361	23	1.3	287	3	US-09-814-353-12588	Sequence 12588, A
C 289	23	1.3	253	8	US-10-357-930-8172	Sequence 8172, A	C 362	23	1.3	287	9	US-10-950-009-31	Sequence 31, Appl
C 290	23	1.3	254	8	US-10-357-930-36011	Sequence 36011, A	C 363	23	1.3	288	3	US-09-732-560-6	Sequence 6, Appl
C 291	23	1.3	255	3	US-09-930-213-570	Sequence 570, Appl	C 364	23	1.3	288	3	US-09-814-353-17819	Sequence 17819, A
C 292	23	1.3	255	8	US-10-357-930-37790	Sequence 37790, A	C 365	23	1.3	289	3	US-09-814-353-4181	Sequence 4181, A
C 293	23	1.3	255	8	US-10-357-930-37965	Sequence 37965, A	C 366	23	1.3	289	3	US-09-814-353-10487	Sequence 10487, A
C 294	23	1.3	257	3	US-09-814-353-18625	Sequence 18625, A	C 367	23	1.3	289	3	US-09-814-353-17249	Sequence 17249, A
C 295	23	1.3	257	8	US-10-425-115-80930	Sequence 80930, A	C 368	23	1.3	289	9	US-10-950-009-231	Sequence 231, Appl
C 296	23	1.3	257	8	US-10-357-930-35960	Sequence 35960, A	C 369	23	1.3	290	8	US-10-357-930-6720	Sequence 6720, A
C 297	23	1.3	258	3	US-09-814-353-4717	Sequence 4717, A	C 370	23	1.3	291	8	US-10-425-115-141495	Sequence 141495, A
C 298	23	1.3	258	3	US-09-814-353-5260	Sequence 5260, A	C 371	23	1.3	291	8	US-10-357-930-37892	Sequence 37892, A
C 299	23	1.3	258	3	US-09-814-353-11015	Sequence 11015, A	C 372	23	1.3	292	8	US-10-357-930-7817	Sequence 7817, A
C 300	23	1.3	258	3	US-09-814-353-11547	Sequence 11547, A	C 373	23	1.3	292	8	US-09-814-353-4787	Sequence 4787, A
C 301	23	1.3	258	8	US-10-357-930-37330	Sequence 37330, A	C 374	23	1.3	293	3	US-09-814-353-11084	Sequence 11084, A
C 302	23	1.3	259	8	US-10-357-930-37636	Sequence 37636, A	C 375	23	1.3	293	3	US-09-732-560-118	Sequence 118, Appl
C 303	23	1.3	259	9	US-10-950-009-959	Sequence 959, Appl	C 376	23	1.3	295	3	US-09-814-353-5669	Sequence 5669, A
C 304	23	1.3	260	3	US-09-814-353-5564	Sequence 5564, A	C 377	23	1.3	295	3	US-09-814-353-11954	Sequence 11954, A
C 305	23	1.3	260	3	US-09-814-353-11851	Sequence 11851, A	C 378	23	1.3	295	6	US-10-125-968-1094	Sequence 1094, A
C 306	23	1.3	260	8	US-10-357-930-37385	Sequence 37385, A	C 379	23	1.3	296	3	US-09-814-353-4475	Sequence 4475, A
C 307	23	1.3	261	3	US-09-814-353-3841	Sequence 3841, A	C 380	23	1.3	296	3	US-09-814-353-5940	Sequence 5940, A
C 308	23	1.3	261	3	US-09-814-353-10150	Sequence 10150, A	C 381	23	1.3	296	3	US-09-814-353-10778	Sequence 10778, A
C 309	23	1.3	263	3	US-09-814-353-4636	Sequence 4636, A	C 382	23	1.3	296	3	US-09-814-353-18220	Sequence 18220, A
C 310	23	1.3	263	3	US-09-814-353-10935	Sequence 10935, A	C 383	23	1.3	297	3	US-09-814-353-12404	Sequence 12404, A
C 311	23	1.3	264	3	US-09-814-353-5108	Sequence 5108, A	C 384	23	1.3	297	8	US-10-357-930-6648	Sequence 6648, A
C 312	23	1.3	264	3	US-09-814-353-5826	Sequence 5826, A	C 385	23	1.3	298	3	US-09-814-353-3017	Sequence 3017, A
C 313	23	1.3	264	3	US-09-814-353-11400	Sequence 11400, A	C 386	23	1.3	298	3	US-09-814-353-9345	Sequence 9345, A
C 314	23	1.3	264	3	US-09-814-353-12108	Sequence 12108, A	C 387	23	1.3	298	8	US-10-357-930-38068	Sequence 38068, A
C 315	23	1.3	266	8	US-10-357-930-36058	Sequence 36058, A	C 388	23	1.3	299	3	US-09-814-353-3301	Sequence 3301, A

C 389	23	1.3	299	3	US-09-814-353-3913	Sequence 3913, Ap
C 390	23	1.3	299	3	US-09-814-353-9622	Sequence 9622, Ap
C 391	23	1.3	299	3	US-09-814-353-10221	Sequence 10221, A
C 392	23	1.3	299	8	US-10-357-930-7675	Sequence 7675, Ap
C 393	23	1.3	300	3	US-09-814-353-5403	Sequence 5403, Ap
C 394	23	1.3	300	3	US-09-814-353-11690	Sequence 11690, A
C 395	23	1.3	300	3	US-09-814-353-12746	Sequence 12746, A
C 396	23	1.3	300	8	US-10-357-930-7819	Sequence 7819, Ap
C 397	23	1.3	301	3	US-09-814-353-3454	Sequence 3454, Ap
C 398	23	1.3	301	8	US-10-425-115-140765	Sequence 140765, A
C 399	23	1.3	302	8	US-10-357-930-7745	Sequence 7745, Ap
C 400	23	1.3	303	3	US-09-814-353-4270	Sequence 4270, Ap
C 401	23	1.3	303	3	US-09-814-353-10574	Sequence 10574, A
C 402	23	1.3	304	3	US-09-814-353-4918	Sequence 4918, Ap
C 403	23	1.3	304	3	US-09-814-353-11212	Sequence 11212, A
C 404	23	1.3	304	8	US-10-357-930-7356	Sequence 7356, Ap
C 405	23	1.3	304	8	US-10-357-930-37545	Sequence 37545, A
C 406	23	1.3	305	3	US-09-814-353-4252	Sequence 4252, Ap
C 407	23	1.3	305	3	US-09-814-353-10556	Sequence 10556, A
C 408	23	1.3	306	8	US-10-357-930-37684	Sequence 37684, A
C 409	23	1.3	308	3	US-09-732-560-47	Sequence 47, Appl
C 410	23	1.3	308	3	US-09-814-353-3733	Sequence 3733, Ap
C 411	23	1.3	308	3	US-09-814-353-10044	Sequence 10044, A
C 412	23	1.3	309	3	US-09-814-353-3152	Sequence 3152, Ap
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C 414	23	1.3	309	3	US-09-814-353-5601	Sequence 5601, Ap
C 415	23	1.3	309	3	US-09-814-353-9477	Sequence 9477, Ap
C 416	23	1.3	309	3	US-09-814-353-11571	Sequence 11571, A
C 417	23	1.3	309	3	US-09-814-353-11888	Sequence 11888, A
C 418	23	1.3	309	3	US-09-814-353-17157	Sequence 17157, A
C 419	23	1.3	310	3	US-09-732-560-52	Sequence 52, Appl
C 420	23	1.3	311	8	US-10-425-115-91139	Sequence 91139, A
C 421	23	1.3	311	9	US-10-950-009-43	Sequence 43, Appl
C 422	23	1.3	313	3	US-09-814-353-6071	Sequence 6071, Ap
C 423	23	1.3	313	3	US-09-814-353-12350	Sequence 12350, A
C 424	23	1.3	313	3	US-09-814-353-18398	Sequence 18398, A
C 425	23	1.3	314	3	US-09-814-353-6050	Sequence 6050, Ap
C 426	23	1.3	314	3	US-09-814-353-12329	Sequence 12329, A
C 427	23	1.3	314	3	US-09-814-353-17831	Sequence 17831, A
C 428	23	1.3	314	6	US-10-125-968-1301	Sequence 1301, Ap
C 429	23	1.3	314	8	US-10-357-930-5890	Sequence 5890, Ap
C 430	23	1.3	315	3	US-09-814-353-4531	Sequence 4531, Ap
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C 432	23	1.3	316	3	US-09-814-353-16036	Sequence 16036, A
C 433	23	1.3	316	3	US-09-814-353-17514	Sequence 17514, A
C 434	23	1.3	316	3	US-09-969-034-30	Sequence 30, Appl
C 435	23	1.3	317	3	US-09-732-560-50	Sequence 50, Appl
C 436	23	1.3	317	3	US-09-814-353-3060	Sequence 3060, Ap
C 437	23	1.3	317	3	US-09-814-353-5587	Sequence 5587, Ap
C 438	23	1.3	317	3	US-09-814-353-9388	Sequence 9388, Ap
C 439	23	1.3	317	3	US-09-814-353-11874	Sequence 11874, A
C 440	23	1.3	318	3	US-09-814-353-4534	Sequence 4534, Ap
C 441	23	1.3	318	3	US-09-814-353-4640	Sequence 4640, Ap
C 442	23	1.3	318	3	US-09-814-353-10835	Sequence 10835, A
C 443	23	1.3	318	3	US-09-814-353-10939	Sequence 10939, A
C 444	23	1.3	318	8	US-10-357-930-7431	Sequence 7431, Ap
C 445	23	1.3	321	3	US-09-814-353-3840	Sequence 3840, Ap
C 446	23	1.3	321	3	US-09-814-353-3987	Sequence 3987, Ap
C 447	23	1.3	321	3	US-09-814-353-10149	Sequence 10149, A
C 448	23	1.3	321	8	US-10-357-930-6795	Sequence 6795, Ap
C 449	23	1.3	321	8	US-10-357-930-37428	Sequence 37428, A
C 450	23	1.3	322	3	US-09-732-560-4	Sequence 4, Appl
C 451	23	1.3	322	3	US-09-814-353-3674	Sequence 3674, Ap
C 452	23	1.3	322	3	US-09-814-353-9987	Sequence 9987, Ap
C 453	23	1.3	323	3	US-09-814-353-17503	Sequence 17503, A
C 454	23	1.3	323	6	US-10-125-968-1376	Sequence 1376, Ap
C 455	23	1.3	324	3	US-09-814-353-4089	Sequence 4089, Ap
C 456	23	1.3	324	3	US-09-814-353-4662	Sequence 4662, Ap
C 457	23	1.3	324	3	US-09-814-353-5754	Sequence 5754, Ap
C 458	23	1.3	324	3	US-09-814-353-6047	Sequence 6047, Ap
C 459	23	1.3	324	3	US-09-814-353-10395	Sequence 10395, A
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			324	3	US-09-814-353-12326	Sequence 12326, A

C 462	23	1.3	324	3	US-09-814-353-18933	Sequence 18933, A
C 463	23	1.3	324	8	US-10-357-930-36148	Sequence 36148, A
C 464	23	1.3	325	3	US-09-834-975-472	Sequence 472, App
C 465	23	1.3	325	3	US-09-814-353-4380	Sequence 4380, Ap
C 466	23	1.3	325	3	US-09-814-353-10684	Sequence 10684, A
C 467	23	1.3	326	3	US-09-814-353-4772	Sequence 4772, Ap
C 468	23	1.3	326	3	US-09-814-353-11069	Sequence 11069, A
C 469	23	1.3	326	3	US-09-814-353-16703	Sequence 16703, A
C 470	23	1.3	326	3	US-09-814-353-18362	Sequence 18362, A
C 471	23	1.3	327	3	US-09-814-353-3345	Sequence 3545, Ap
C 472	23	1.3	327	3	US-09-814-353-5917	Sequence 5917, Ap
C 473	23	1.3	327	3	US-09-814-353-9859	Sequence 9859, Ap
C 474	23	1.3	327	3	US-09-814-353-12198	Sequence 12198, A
C 475	23	1.3	327	3	US-09-814-353-17232	Sequence 17232, A
C 476	23	1.3	327	8	US-10-357-930-8158	Sequence 8158, Ap
C 477	23	1.3	327	8	US-10-357-930-8158	Sequence 8158, Ap
C 478	23	1.3	328	3	US-09-814-353-18726	Sequence 18726, A
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C 480	23	1.3	329	3	US-09-814-353-4341	Sequence 4341, Ap
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C 482	23	1.3	329	3	US-09-814-353-17483	Sequence 17483, A
C 483	23	1.3	329	8	US-10-357-930-7690	Sequence 7690, Ap
C 484	23	1.3	329	9	US-10-950-009-593	Sequence 593, App
C 485	23	1.3	330	3	US-09-814-353-4620	Sequence 4620, Ap
C 486	23	1.3	330	3	US-09-814-353-5482	Sequence 5482, Ap
C 487	23	1.3	330	3	US-09-814-353-10919	Sequence 10919, A
C 488	23	1.3	330	3	US-09-814-353-11769	Sequence 11769, A
C 489	23	1.3	330	3	US-09-814-353-17646	Sequence 17646, A
C 490	23	1.3	330	3	US-09-814-353-18207	Sequence 18207, A
C 491	23	1.3	330	8	US-10-357-930-9103	Sequence 9103, Ap
C 492	23	1.3	331	3	US-09-814-353-4327	Sequence 4327, Ap
C 493	23	1.3	331	3	US-09-814-353-10631	Sequence 10631, A
C 494	23	1.3	332	3	US-09-814-353-3601	Sequence 3601, Ap
C 495	23	1.3	332	3	US-09-814-353-5594	Sequence 5594, Ap
C 496	23	1.3	332	3	US-09-814-353-9915	Sequence 9915, Ap
C 497	23	1.3	332	3	US-09-814-353-11881	Sequence 11881, A
C 498	23	1.3	333	3	US-09-814-353-4698	Sequence 4698, Ap
C 499	23	1.3	333	3	US-09-814-353-10997	Sequence 10997, A
C 500	23	1.3	333	3	US-09-814-353-16634	Sequence 16634, A

ALIGNMENTS

RESULT 1

US-09-989-890-105
; Sequence 105, Application US/09989890
; Publication No. US20040166105A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Pluta, Jason
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pro
; FILE REFERENCE: DEX-0287
; CURRENT APPLICATION NUMBER: US/09/989,890
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,509
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-890-105

Query Match 100.0%; Score 1713; DB 3; Length 1713;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGCCCCGCTGGACACACCCCGCCAGCATCTGGGCTCCACGCTTGGACCGTGGAG 60
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Db 241 TGGGTGTGGAGTGTGTGCGGGCTGCTTCTGCTTCCGCGCTGCGGGATTCCTCCAG 300
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RESULT 2
US-10-104-047-799
; Sequence 799, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 799
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-799

Query Match 93.1%; Score 1594; DB 6; Length 1785;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1681 CACAGTTGTAAAGTAC 1696
Db 1770 CACAGTTGTAAAGTAC 1785

RESULT 3

US-09-989-920-56
; Sequence 56, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-56

Query Match 57.4%; Score 983; DB 3; Length 1977;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1103; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 598 CACAGCTGCCCAGACACCTTTGCCAGTAGTCTCTCGTGGCTCCGAGAGTACTATTCTTTC 657
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Qy 658 CATGAGTGGACCTCGACCTGCCGAGATGGGAGTGGCTCCATGTGCGAGCCGAGAAAT 717

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QY 1437 GTCTTCAGGTGGCTGATCATGGAAGTAAGAGTTAGGATTAACCTTCTGGAGTGAAC 1496
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QY 1617 CACTCTATGTTATGTTAAGAGTTGGTTCTTGCTTCTGGCTGATGTTCTGTATCTTAACA 1676
Db 1881 CACTCTATGTTATGTTAAGAGTTGGTTCTTGCTTCTGGCTGATGTTCTGTATCTTAACA 1940
QY 1677 TGACCACAGTTTGTAAAGTACCTCG 1700
Db 1941 TGACCACAGTTTGTAAAGTACCTCG 1964

RESULT 5
US-09-989-920-55
; Sequence 55, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Pro
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-55

Query Match 22.5%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.5e-194; Indels 0; Gaps 0;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1190 ACTGCTAAACCCCTGCCAGGCCACAGCTGCCACACCCCTTTCTGGGAGAGCATGSCCTACAG 1249
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Db 121 CTGGCTCCTCTGCTGCTGGTCTGACTGGGTTCTTGACCACTGTCATTTCACTGGGGCATTG 180
QY 1370 GGATCTACATCTCCTTGCATTCCTCCAGCTGCTGATCCCTGCCAGGGCCCTTCCTTCCT 1429
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RESULT 6
US-09-989-890-104
; Sequence 104, Application US/09989890
; Publication No. US20040166105A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Pluta, Jason
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pro
; FILE REFERENCE: DEX-0287
; CURRENT APPLICATION NUMBER: US/09/989,890
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,509
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 386
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-890-104

Query Match 22.1%; Score 378; DB 3; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.4e-190; Indels 0; Gaps 0;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1203 GCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGGCCTACAGAATGAAGAGGGG 1262
Db 9 GCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGGCCTACAGAATGAAGAGGGG 68
QY 1263 ACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCTCTGGGCTCTCTCTG 1322
Db 69 ACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCTCTGGGCTCTCTCTG 128
QY 1323 CTTGGCTGACTGGGTTCTTGACCATGTGCAATTTCACTGGGGCATGGGATCTACATCTC 1382
Db 129 CTTGGCTGACTGGGTTCTTGACCATGTGCAATTTCACTGGGGCATGGGATCTACATCTC 188
QY 1383 CTTGATCCCCAGCTGGTCTGATCCCTGCCAGGGCCCTTCTTCTGCTCATGTGCTTC 1442
Db 189 CTTGATCCCCAGCTGGTCTGATCCCTGCCAGGGCCCTTCTTCTGCTCATGTGCTTC 248
QY 1443 AGTGGCCCTGATCATGGAAGTAAGAGTTAGGCATTACCTTTCTGGGAGTGAACCCCTGAC 1502
Db 249 AGTGGCCCTGATCATGGAAGTAAGAGTTAGGCATTACCTTTCTGGGAGTGAACCCCTGAC 308
QY 1503 TGCATCCCCCTATTGGCACCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAATTC 1562
Db 309 TGCATCCCCCTATTGGCACCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAATTC 368
QY 1563 AACAGTTAAAGAAGCTT 1580
Db 369 AACAGTTAAAGAAGCTT 386

RESULT 7


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; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 12051
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 401
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-12051
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Query Match      18.7%; Score 321; DB 9; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.6e-160;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCGCGCTGAGACACCCGCCAGCATCTGGGCTCCAGCTTGGAGCCGTGGAG 60
DB 80 ATGCCCGCGCTGAGACACCCGCCAGCATCTGGGCTCCAGCTTGGAGCCGTGGAG 139

QY 61 CGGCCAACAGAGATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCAGCCGC 120
DB 140 CGGCCAACAGAGATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCAGCCGC 199

QY 121 CGCACCGGTAGACAGACCCAGGACCTTGGCCACCATGAGGCGGACAGAGCATTACCTTC 180
DB 200 CGCACCGGTAGACAGACCCAGGACCTTGGCCACCATGAGGCGGACAGAGCATTACCTTC 259

QY 181 ATCTCTGGCTCTGCTGAGCGCGGCTTGTAGTCCCCACCTGTGCTGCTGCTGCGGACCC 240
DB 260 ATCTCTGGCTCTGCTGAGCGGCTTGTAGTCCCCACCTGTGCTGCTGCTGCGGACCC 319

QY 241 TGGGTGTGGAGTGTGTGCGGGTGTGCTTGTCTTCCGCGCTGCGGGATTCCTCCAG 300
DB 320 TGGGTGTGGAGTGTGTGCGGGTGTGCTTGTCTTCCGCGCTGCGGGATTCCTCCAG 379

QY 301 CGCTGTGGAGCTGTGTGCGG 321
DB 380 CGCTGTGGAGCTGTGTGCGG 400
```

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RESULT 10
US-10-779-543-1705
; Sequence 1705, Application US/10779543
; Publication No. US2005027917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: US/10/779,543
; PRIOR FILING DATE: 2002-02-15
```

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; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 1705
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-779-543-1705

Query Match      17.5%; Score 300; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 6.1e-149;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 825 CTCGGACCTTATCAGCAGCATCAGCAGGATCAGCAGGATACACCTGGATGAGCAGGATCTCAGGG 884
DB 1 CTCGGACCTTATCAGCAGCATCAGCAGGATCAGCAGGATACACCTGGATGAGCAGGATCTCAGGG 60

QY 885 CGGCCTGTGTACGCGGCATCATTCGCATTAGTAGTACCCGAAAGAGCCGTGCTCGCCACAGAC 944
DB 61 CGGCCTGTGTACGCGGCATCATTCGCATTAGTAGTACCCGAAAGAGCCGTGCTCGCCACAGAC 120

QY 945 CTCGGAGGTGTGTTCAACTCGGGCTGTCTGCCCAACCGCTGTGCCCTTGACAGTGGCCA 1004
DB 121 CTCGGAGGTGTGTTCAACTCGGGCTGTCTGCCCAACCGCTGTGCCCTTGACAGTGGCCA 180

QY 1005 TGAGACCATGTGGGCTCAGGTCAGCCAGAGATGAGCTGACAGTGCAGATCTCCAGGA 1064
DB 181 TGAGACCATGTGGGCTCAGGTCAGCCAGAGATGAGCTGACAGTGCAGATCTCCAGGA 240

QY 1065 GACGACTGCAGATGCCATCGCCGGAAGCTGAGGCTTATGGAGCTTCCAGGTTACCCAGC 1124
DB 241 GACGACTGCAGATGCCATCGCCGGAAGCTGAGGCTTATGGAGCTTCCAGGTTACCCAGC 300

RESULT 11
US-10-076-555-34
; Sequence 34, Application US/10076555
; Publication No. US20030065156A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominiguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kaseam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
```

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; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Novel Human Genes and Gene Expression
; TITLE OF INVENTION: Products I
; FILE REFERENCE: 2300-1480
; CURRENT APPLICATION NUMBER: US/10/076,555
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,877
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-555-34

Query Match 14.5%; Score 249; DB 5; Length 300;
Best Local Similarity 99.7%; Pred. No. 1e-121;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGACAGAGCTGTTTCAGCGTACACAGATCGATGAGCTGGCCAAAGTGCACATCAGACACTG 799
Db 1 TGACAGAGCTGTTTCAGCGTACACAGATCGATGAGCTGGCCAAAGTGCACATCAGACACTG 60

QY 800 TGTTCTCGGAGAGACAGTAAGATCTCGACCTTATCAGACGATCACCAGGACTACC 859
Db 61 TGTTCTCGGAGAGACAGTAAGATCTCGACCTTATCAGACGATCACCAGGACTACC 120

QY 860 ACCTGATGAGCAGGATGCTGAGGGCGCCTGTGACGCGCATCTTCGATTAGTACC 919
Db 121 ACCTGATGAGCAGGATGCTGAGGGCGCCTGTGACGCGCATCTTCGATTAGTACC 180

QY 920 GAAAGAGCGGTGCTCGCCACAGACCTCGAGAGGTGTTCAACTCGGGCTGCTGCCCAA 979
Db 181 GAAAGAGCGGTGCTCGCCACAGACCTCGAGAGGTGTTCAACTCGGGCTGCTGCCCAA 240

QY 980 CCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGCTTCAGCCAGATG 1039
Db 241 CCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGCTTCAGCCAGATG 300

RESULT 12
US-10-779-543-34
; Sequence 34, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03

Query Match 14.5%; Score 249; DB 9; Length 300;
Best Local Similarity 99.7%; Pred. No. 1e-121;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGACAGAGCTGTTTCAGCGTACACAGATCGATGAGCTGGCCAAAGTGCACATCAGACACTG 799
Db 1 TGACAGAGCTGTTTCAGCGTACACAGATCGATGAGCTGGCCAAAGTGCACATCAGACACTG 60

QY 800 TGTTCTCGGAGAGACAGTAAGATCTCGACCTTATCAGACGATCACCAGGACTACC 859
Db 61 TGTTCTCGGAGAGACAGTAAGATCTCGACCTTATCAGACGATCACCAGGACTACC 120

QY 860 ACCTGATGAGCAGGATGCTGAGGGCGCCTGTGACGCGCATCTTCGATTAGTACC 919
Db 121 ACCTGATGAGCAGGATGCTGAGGGCGCCTGTGACGCGCATCTTCGATTAGTACC 180

QY 920 GAAAGAGCGGTGCTCGCCACAGACCTCGAGAGGTGTTCAACTCGGGCTGCTGCCCAA 979
Db 181 GAAAGAGCGGTGCTCGCCACAGACCTCGAGAGGTGTTCAACTCGGGCTGCTGCCCAA 240

QY 980 CCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGCTTCAGCCAGATG 1039
Db 241 CCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGCTTCAGCCAGATG 300

RESULT 13
US-10-074-475-124
; Sequence 124, Application US/10074475
; Publication No. US20030092898A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Karra, Kalpana
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
; TITLE OF INVENTION: Genes and Proteins
; FILE REFERENCE: DEX-0313
; CURRENT APPLICATION NUMBER: US/10/074,475
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,292
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-074-475-124
```



```
Db      1  GATGTTAAGCTCRAAGGCATCCCTG 25

RESULT 17
US-10-131-827-8473
; Sequence 8473, Application US/10131827
; Publication No. US2004009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8473
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(224)
; OTHER INFORMATION: n = A, C, T or G
US-10-131-827-8473

Query Match      1.5%; Score 25; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1689  GTAAGTACCTCGCGCGGACACGC 1713
Db      189  GTAAGTACCTCGCGCGGACACGC 213

RESULT 18
US-10-357-930-37484/c
; Sequence 37484, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR FILING DATE: 2003-02-16
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37484

Query Match      1.5%; Score 25; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1689  GTAAGTACCTCGCGCGGACACGC 1713
Db      189  GTAAGTACCTCGCGCGGACACGC 213

RESULT 19
US-09-814-353-17410/c
; Sequence 17410, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17410
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-17410

Query Match      1.5%; Score 25; DB 3; Length 275;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1689  GTAAGTACCTCGCGCGGACACGC 1713
Db      87  GTAAGTACCTCGCGCGGACACGC 63

RESULT 20
US-10-357-930-7524/c
; Sequence 7524, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
```

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; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-37484

Query Match      1.5%; Score 25; DB 8; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1689  GTAAGTACCTCGCGCGGACACGC 1713
Db      97  GTAAGTACCTCGCGCGGACACGC 73

RESULT 19
US-09-814-353-17410/c
; Sequence 17410, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17410
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-17410

Query Match      1.5%; Score 25; DB 3; Length 275;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1689  GTAAGTACCTCGCGCGGACACGC 1713
Db      87  GTAAGTACCTCGCGCGGACACGC 63

RESULT 20
US-10-357-930-7524/c
; Sequence 7524, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
```

; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7524
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 123, 131, 149, 152, 166, 201, 284
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-7524

Query Match 1.5%; Score 25; DB 8; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACCTCGCGCGGACCGC 1713
DB 39 GTAAGTACCTCGCGCGGACCGC 15

RESULT 21

US-09-814-353-5095
; Sequence 5095, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B

; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5095
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-5095

Query Match 1.5%; Score 25; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACCTCGCGCGGACCGC 1713

DB 280 GTAAGTACCTCGCGCGGACCGC 304

RESULT 22

US-09-814-353-11387
; Sequence 11387, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11387
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-11387

Query Match 1.5%; Score 25; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACCTCGCGCGGACCGC 1713
DB 280 GTAAGTACCTCGCGCGGACCGC 304

RESULT 23

US-10-060-036-4393
; Sequence 4393, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4393
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-4393

Query Match 1.5%; Score 25; DB 5; Length 453;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1689 GTAAGTACCTCGCGCGGACACGC 1713
Db 428 GTAAGTACCTCGCGCGGACACGC 452

RESULT 24
US-09-814-353-17771
; Sequence 17771, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17771
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-17771

Query Match 1.5%; Score 25; DB 3; Length 463;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACCTCGCGCGGACACGC 1713
Db 351 GTAAGTACCTCGCGCGGACACGC 375

RESULT 25
US-10-074-511-10/c
; Sequence 10, Application US/10074511
; Publication No. US20030176672A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Karra, Kalpana
; APPLICANT: Caferkey, Robert
; APPLICANT: Liu, Chenghua
; APPLICANT: Sun, Yongming
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and
; FILE REFERENCE: DEX-0314
; CURRENT APPLICATION NUMBER: US/10/074,511
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,289
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 810
; TYPE: DNA
```

```
; ORGANISM: Homo sapien
US-10-074-511-10

Query Match 1.5%; Score 25; DB 6; Length 810;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACCTCGCGCGGACACGC 1713
Db 25 GTAAGTACCTCGCGCGGACACGC 1

RESULT 26
US-10-198-846-5605/c
; Sequence 5605, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5605
; LENGTH: 1252
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 3, 4, 5, 14, 18, 19, 20, 22, 26, 28, 29, 35, 36, 42, 46,
; LOCATION: 48, 50, 51, 52, 57, 58, 60, 62, 63, 64, 77, 81, 83, 90,
; LOCATION: 93, 96, 99, 102, 103, 107, 115, 116, 121, 124, 127, 146,
; LOCATION: 169, 382, 433, 437, 465, 473, 480, 498, 517, 539, 541, 572
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 577, 591, 610, 627, 628, 657, 664, 672, 709, 712, 720, 726,
; LOCATION: 732, 734, 738, 753, 756, 772, 783, 789, 790, 797, 813, 814,
; LOCATION: 815, 830, 835, 837, 846, 864, 868, 873, 877, 896, 903, 921,
; LOCATION: 925, 926, 928, 936, 941, 957, 958, 974, 980, 985, 986
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 991, 996, 997, 999, 1001, 1002, 1008, 1010, 1015, 1018, 1019,
; LOCATION: 1025, 1029, 1031, 1039, 1040, 1046, 1048, 1054, 1055, 1059,
; LOCATION: 1060, 1063, 1067, 1068, 1069, 1070, 1072, 1075, 1079, 1080,
; LOCATION: 1085, 1091, 1094, 1097, 1100, 1102, 1105, 1107, 1116
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1126, 1128, 1132, 1137, 1138, 1140, 1141, 1144, 1148, 1151,
; LOCATION: 1156, 1165, 1166, 1173, 1176, 1183, 1188, 1193, 1194, 1195,
; LOCATION: 1199, 1201, 1209, 1212, 1215, 1216, 1220, 1221, 1222, 1223,
; LOCATION: 1224, 1230, 1231, 1239, 1240, 1243, 1244, 1245, 1252
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-5605

Query Match 1.5%; Score 25; DB 5; Length 1252;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACCTCGCGCGGACACGC 1713
Db 224 GTAAGTACCTCGCGCGGACACGC 200
```


RESULT 27

US-10-950-009-1051/c
; Sequence 1051, Application US/10950009
; Publication No. US2005069934A1
; GENERAL INFORMATION:
; APPLICANT: BERKA, Randy
; APPLICANT: BASHKIROVA, Elena
; APPLICANT: REY, Michael
; TITLE OF INVENTION: Methods For Monitoring Gene Expression
; FILE REFERENCE: 10541.200-US
; CURRENT APPLICATION NUMBER: US/10/950,009
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: 60/506,140
; PRIOR FILING DATE: 2003-09-25
; NUMBER OF SEQ ID NOS: 1190
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1051
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Trichoderma reesei
US-10-950-009-1051

Query Match 1.4%; Score 24; DB 9; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCCGCGACACGC 1713
|||
DB 24 TAAGTACCTCGGCCGCGACACGC 1

RESULT 28

US-10-477-445-15
; Sequence 15, Application US/10477445
; Publication No. US20050130138A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: Immune-related proteins and the regulation of the same
; FILE REFERENCE: RCK-12
; CURRENT APPLICATION NUMBER: US/10/477,445
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: PCT/EP02/05127
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/290,312
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 111
; SEQ ID NO 15
; LENGTH: 232
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 145..145
; OTHER INFORMATION: unknown nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 231..231
; OTHER INFORMATION: unknown nucleotide
US-10-477-445-15

Query Match 1.4%; Score 24; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACTCGGCCGCGACAC 1711
|||
DB 207 TGTAACTACTCGGCCGCGACAC 230

RESULT 29

US-09-814-353-17222/c
; Sequence 17222, Application US/09814353

; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17222
; LENGTH: 253
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-17222

Query Match 1.4%; Score 24; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCCGCGACACGC 1713
|||
DB 77 TAAGTACCTCGGCCGCGACACGC 54

RESULT 30

US-09-814-353-5345/c
; Sequence 5345, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5345
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-5345

Query Match 1.4%; Score 24; DB 3; Length 274;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 31

US-09-814-353-11632/c
; Sequence 11632, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11632
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-814-353-11632

Query Match 1.4%; Score 24; DB 3; Length 274;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 32

US-09-814-353-16395/c
; Sequence 16395, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16395
; LENGTH: 283
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-16395

Query Match 1.4%; Score 24; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 54 TAAGTACCTCGCGCGGACACGC 31

RESULT 33

US-09-814-353-3678/c
; Sequence 3678, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3678
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-814-353-3678

Query Match 1.4%; Score 24; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 34

US-09-814-353-9991/c
; Sequence 9991, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela

```
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9991
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-9991

Query Match          1.4%; Score 24; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 35
US-09-814-353-4074/c
; Sequence 4074, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4074
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-4074

Query Match          1.4%; Score 24; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 36
US-09-814-353-10381/c
; Sequence 10381, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10381
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-10381

Query Match          1.4%; Score 24; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 37
US-09-814-353-2976/c
; Sequence 2976, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
```

; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2976
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 181, 183, 191, 314
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-2976

Query Match 1.4%; Score 24; DB 3; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGGCACACGC 1713
|||||
DB 30 TAAGTACCTCGCGGCACACGC 7

RESULT 38

US-09-814-353-9305/c
; Sequence 9305, Application US/09814353
; Publication No. US20030165831A1

; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9305
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 181, 183, 191, 314
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-9305

Query Match 1.4%; Score 24; DB 3; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGGCACACGC 1713
|||||
DB 30 TAAGTACCTCGCGGCACACGC 7

RESULT 39

US-09-969-034-1870
; Sequence 1870, Application US/09969034

; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poornima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; TITLE OF INVENTION: Expressed in Cancer Tissue
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1870
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 259
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-1870

Query Match 1.4%; Score 24; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGGCACACGC 1713
|||||
DB 289 TAAGTACCTCGCGGCACACGC 312

RESULT 40

US-09-814-353-17947/c
; Sequence 17947, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17947
; LENGTH: 326
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 114

QY 1690 TAAGTACCTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 44

US-09-814-353-5958/c
; Sequence 5958, Application US/09814353
; Publication No. US2003016581A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5958
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 236, 252, 254, 313, 322, 329
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-5958

Query Match 1.4%; Score 24; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 45

US-09-814-353-12238/c
; Sequence 12238, Application US/09814353
; Publication No. US2003016581A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820

; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12238
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 236, 252, 254, 313, 322, 329
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-12238

Query Match 1.4%; Score 24; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 46

US-10-357-930-6066/c
; Sequence 6066, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6066
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-6066

Query Match 1.4%; Score 24; DB 8; Length 376;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 47

US-09-814-353-16765/c

```
; Sequence 16765, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16765
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-16765

Query Match 1.4%; Score 24; DB 3; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 101 TAAGTACCTCGGCGGACACGC 78

RESULT 48
US-09-814-353-2902/c
; Sequence 2902, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2902
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
US-09-814-353-2902

Query Match 1.4%; Score 24; DB 3; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 30 TAAGTACCTCGGCGGACACGC 7

RESULT 49
US-09-814-353-9231/c
; Sequence 9231, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9231
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-9231

Query Match 1.4%; Score 24; DB 3; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 30 TAAGTACCTCGGCGGACACGC 7

RESULT 50
US-09-814-353-16375/c
; Sequence 16375, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16375
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```

; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version.4.0
; SEQ ID NO 16375
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-16375

Query Match      1.4%; Score 24; DB 3; Length 391;
Best Local Similarity 100.0%; Pred.No.0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1690 TAAGTACTCGCGCGGACGACGCG 1713
          |||||||
Db      110 TAAGTACTCGCGCGGACGACGCG 87

RESULT 51
US-09-814-353-3267/c
; Sequence 3267, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3267
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 327, 378, 384
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-3267

Query Match      1.4%; Score 24; DB 3; Length 392;
Best Local Similarity 100.0%; Pred.No.0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1690 TAAGTACTCGCGCGGACGACGCG 1713
          |||||||
Db      30 TAAGTACTCGCGCGGACGACGCG 7

RESULT 52
US-09-814-353-9592/c

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```
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8043
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 37, 54, 147
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-8043

Query Match          1.4%; Score 24; DB 8; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCTCGCGCGGACACGC 1713
Db 30 TAAGTACTCTCGCGCGGACACGC 7

RESULT 54
US-09-814-353-16049/c
; Sequence 16049, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16049
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-16049

Query Match          1.4%; Score 24; DB 3; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCTCGCGCGGACACGC 1713
Db 111 TAAGTACTCTCGCGCGGACACGC 88

RESULT 55
US-09-814-353-17159/c
; Sequence 17159, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
```

```
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17159
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-17159

Query Match          1.4%; Score 24; DB 3; Length 415;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACTCTCGCGCGGACACGC 1713
Db 111 TAAGTACTCTCGCGCGGACACGC 88

RESULT 56
US-09-814-353-5221/c
; Sequence 5221, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5221
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 271
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-5221

Query Match          1.4%; Score 24; DB 3; Length 416;
```

```
Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
    |||||
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 57
US-09-814-353-11508/c
; Sequence 11508, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11508
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 271
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-11508

Query Match 1.4%; Score 24; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
    |||||
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 58
US-09-814-353-12779
; Sequence 12779, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15689
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-15689

Query Match 1.4%; Score 24; DB 3; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1690 TAAGTACCTCGCGCGGACACGC 1713
    |||||
Db 391 TAAGTACCTCGCGCGGACACGC 414

RESULT 59
US-09-814-353-15689/c
; Sequence 15689, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15689
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-15689

Query Match 1.4%; Score 24; DB 3; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
    |||||
Db 111 TAAGTACCTCGCGCGGACACGC 88

RESULT 60
US-09-814-353-5813
; Sequence 5813, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5813
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-5813

Query Match      1.4%; Score 24; DB 3; Length 421;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713
DB 391 TAAGTACCTCGCGCGACACGC 414
|||||
; US-10-357-930-39249/c
; Sequence 39249, Application US/10/357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39249
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-357-930-39249
```

```
Query Match      1.4%; Score 24; DB 8; Length 424;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713
DB 85 TAAGTACCTCGCGCGACACGC 62
|||||
; US-10-198-846-7580/c
; Sequence 7580, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7580
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 384
; OTHER INFORMATION: n = A,T,C or G
; US-10-198-846-7580

Query Match      1.4%; Score 24; DB 5; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713
DB 105 TAAGTACCTCGCGCGACACGC 82
|||||
; US-09-814-353-18496/c
; Sequence 18496, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
```

```
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18496
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-18496

Query Match      1.4%; Score 24; DB 3; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACCAACGC 1713
Db 111 TAAGTACCTCGGCGGACCAACGC 88

RESULT 64
US-10-357-930-6566/c
; Sequence 6566, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6566
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-6566

Query Match      1.4%; Score 24; DB 8; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACCAACGC 1713
Db 30 TAAGTACCTCGGCGGACCAACGC 7

RESULT 65
US-09-814-353-18622/c
; Sequence 18622, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
```

```
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18622
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-18622

Query Match      1.4%; Score 24; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACCAACGC 1713
Db 95 TAAGTACCTCGGCGGACCAACGC 72

RESULT 66
US-10-357-930-37944/c
; Sequence 37944, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37944
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-37944

Query Match      1.4%; Score 24; DB 8; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1690 TAAGTACTCGCGCGACCGC 1713
|||||
Db 56 TAAGTACTCGCGCGACCGC 33

RESULT 67
US-09-814-353-3100/c
; Sequence 3100, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3100
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 182, 223, 225, 281, 285, 392
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-3100

Query Match 1.4%; Score 24; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1690 TAAGTACTCGCGCGACCGC 1713
|||||
Db 30 TAAGTACTCGCGCGACCGC 7

RESULT 68
US-09-814-353-9426/c
; Sequence 9426, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9426
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 182, 223, 225, 281, 285, 392
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-9426

Query Match 1.4%; Score 24; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1690 TAAGTACTCGCGCGACCGC 1713
|||||
Db 30 TAAGTACTCGCGCGACCGC 7

RESULT 69
US-09-814-353-18016/c
; Sequence 18016, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18016
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 182, 223, 225, 281, 285, 392
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-9426

Query Match 1.4%; Score 24; DB 3; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1690 TAAGTACTCGCGCGACCGC 1713
|||||
Db 106 TAAGTACTCGCGCGACCGC 83

RESULT 70
US-09-814-353-15845/c
; Sequence 15845, Application US/09814353
; Publication No. US20030165831A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15845
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-15845

Query Match          1.4%; Score 24; DB 3; Length 444;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCAACGC 1713
DB 73 TAAGTACCTCGCGCGGACCAACGC 50

RESULT 71
US-09-814-353-4306/c
; Sequence 4306, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4306
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature

Query Match          1.4%; Score 24; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCAACGC 1713
DB 73 TAAGTACCTCGCGCGGACCAACGC 50

RESULT 72
US-09-814-353-10610/c
; Sequence 10610, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10610
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature

Query Match          1.4%; Score 24; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCAACGC 1713
DB 30 TAAGTACCTCGCGCGGACCAACGC 7

RESULT 73
US-10-357-930-36059/c
; Sequence 36059, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
```

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; LOCATION: 324
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4306

Query Match          1.4%; Score 24; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCAACGC 1713
DB 30 TAAGTACCTCGCGCGGACCAACGC 7

RESULT 72
US-09-814-353-10610/c
; Sequence 10610, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10610
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature

Query Match          1.4%; Score 24; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCAACGC 1713
DB 30 TAAGTACCTCGCGCGGACCAACGC 7

RESULT 73
US-10-357-930-36059/c
; Sequence 36059, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
```

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; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36059
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-36059

Query Match      1.4%; Score 24; DB 8; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 101 TAAGTACCTCGGCGGACACGC 78

RESULT 74
US-10-357-930-37991/c
; Sequence 37991, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37991
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-37991

Query Match      1.4%; Score 24; DB 8; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 101 TAAGTACCTCGGCGGACACGC 78

US-10-001-857-66/c
; Sequence 66, Application US/10001857
; Publication No. US20020183500A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0273
; CURRENT APPLICATION NUMBER: US/10/001,857
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,054
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-857-66
```

```
Db 71 TAAGTACCTCGGCGGACACGC 48

RESULT 75
US-10-357-930-45120/c
; Sequence 45120, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45120
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-45120

Query Match      1.4%; Score 24; DB 8; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 101 TAAGTACCTCGGCGGACACGC 78

RESULT 76
US-10-001-857-66/c
; Sequence 66, Application US/10001857
; Publication No. US20020183500A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0273
; CURRENT APPLICATION NUMBER: US/10/001,857
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,054
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-857-66
```

```
Query Match      1.4%; Score 24; DB 5; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690 TAAGTACCTCGCGCGGACACGC 1713
Db      24 TAAGTACCTCGCGCGGACACGC 1

RESULT 77
US-09-814-353-18705/c
; Sequence 18705, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18705
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-18705

Query Match      1.4%; Score 24; DB 3; Length 460;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690 TAAGTACCTCGCGCGGACACGC 1713
Db      108 TAAGTACCTCGCGCGGACACGC 85

RESULT 78
US-10-198-846-5501/c
; Sequence 5501, Application US/10198846
; Publication No. US2003099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steimann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5501
; LENGTH: 463
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18, 43, 86, 88, 89, 264, 388, 407, 432
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-5501

Query Match      1.4%; Score 24; DB 5; Length 463;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690 TAAGTACCTCGCGCGGACACGC 1713
Db      116 TAAGTACCTCGCGCGGACACGC 93

RESULT 79
US-09-814-353-3344/c
; Sequence 3344, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3344
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 99, 279, 300, 303, 315, 331, 344, 352, 356, 371, 377, 380,
; LOCATION: 383, 393, 403, 417, 422, 428, 431
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-3344

Query Match      1.4%; Score 24; DB 3; Length 464;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690 TAAGTACCTCGCGCGGACACGC 1713
Db      30 TAAGTACCTCGCGCGGACACGC 7

RESULT 80
US-09-814-353-9665/c
; Sequence 9665, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
```


/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

/ FILE REFERENCE: MRI-006B

/ CURRENT APPLICATION NUMBER: US/09/814,353

/ CURRENT FILING DATE: 2001-03-21

/ PRIOR APPLICATION NUMBER: US 60/191,031

/ PRIOR FILING DATE: 2000-03-21

/ PRIOR APPLICATION NUMBER: US 60/207,124

/ PRIOR FILING DATE: 2000-05-25

/ PRIOR APPLICATION NUMBER: US 60/211,940

/ PRIOR FILING DATE: 2000-06-15

/ PRIOR APPLICATION NUMBER: US 60/216,820

/ PRIOR FILING DATE: 2000-07-07

/ PRIOR APPLICATION NUMBER: US 60/220,661

/ PRIOR FILING DATE: 2000-07-25

/ PRIOR APPLICATION NUMBER: US 60/257,672

/ PRIOR FILING DATE: 2000-12-21

/ NUMBER OF SEQ ID NOS: 22037

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 9665

/ LENGTH: 464

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURE:

/ NAME/KEY: misc feature

/ LOCATION: 99, 279, 300, 303, 315, 331, 344, 352, 356, 371, 377, 380,

/ LOCATION: 383, 393, 403, 417, 422, 428, 431

/ OTHER INFORMATION: n = A,T,C or G

US-09-814-353-9665

Query Match 1.4%; Score 24; DB 3; Length 464;

Best Local Similarity 100.0%; Pred.No. 0.13; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713

Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 81

US-09-814-353-15951/c

/ Sequence 15851, Application US/09814353

/ Publication No. US20030165831A1

/ GENERAL INFORMATION:

/ APPLICANT: Thompson, Pamela

/ APPLICANT: Lillie, James

/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

/ TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

/ FILE REFERENCE: MRI-006B

/ CURRENT APPLICATION NUMBER: US/09/814,353

/ CURRENT FILING DATE: 2001-03-21

/ PRIOR APPLICATION NUMBER: US 60/191,031

/ PRIOR FILING DATE: 2000-03-21

/ PRIOR APPLICATION NUMBER: US 60/207,124

/ PRIOR FILING DATE: 2000-05-25

/ PRIOR APPLICATION NUMBER: US 60/211,940

/ PRIOR FILING DATE: 2000-06-15

/ PRIOR APPLICATION NUMBER: US 60/216,820

/ PRIOR FILING DATE: 2000-07-07

/ PRIOR APPLICATION NUMBER: US 60/220,661

/ PRIOR FILING DATE: 2000-07-25

/ PRIOR APPLICATION NUMBER: US 60/257,672

/ PRIOR FILING DATE: 2000-12-21

/ NUMBER OF SEQ ID NOS: 22037

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 15851

/ LENGTH: 471

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-09-814-353-15951

Query Match 1.4%; Score 24; DB 3; Length 471;

Best Local Similarity 100.0%; Pred.No. 0.13; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713

Db 103 TAAGTACCTCGCGCGACACGC 80

RESULT 82

US-09-814-353-4472/c

/ Sequence 4472, Application US/09814353

/ Publication No. US20030165831A1

/ GENERAL INFORMATION:

/ APPLICANT: Lee, John

/ APPLICANT: Thompson, Pamela

/ APPLICANT: Lillie, James

/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

/ TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

/ FILE REFERENCE: MRI-006B

/ CURRENT APPLICATION NUMBER: US/09/814,353

/ CURRENT FILING DATE: 2001-03-21

/ PRIOR APPLICATION NUMBER: US 60/191,031

/ PRIOR FILING DATE: 2000-03-21

/ PRIOR APPLICATION NUMBER: US 60/207,124

/ PRIOR FILING DATE: 2000-05-25

/ PRIOR APPLICATION NUMBER: US 60/211,940

/ PRIOR FILING DATE: 2000-06-15

/ PRIOR APPLICATION NUMBER: US 60/216,820

/ PRIOR FILING DATE: 2000-07-07

/ PRIOR APPLICATION NUMBER: US 60/220,661

/ PRIOR FILING DATE: 2000-07-25

/ PRIOR APPLICATION NUMBER: US 60/257,672

/ PRIOR FILING DATE: 2000-12-21

/ NUMBER OF SEQ ID NOS: 22037

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 4472

/ LENGTH: 486

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURE:

/ NAME/KEY: misc feature

/ LOCATION: 31, 98, 159, 166, 289, 348, 361, 364, 385, 393, 398, 400,

/ LOCATION: 403, 410, 414, 419, 432, 457, 467

/ OTHER INFORMATION: n = A,T,C or G

US-09-814-353-4472

Query Match 1.4%; Score 24; DB 3; Length 486;

Best Local Similarity 100.0%; Pred.No. 0.13; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713

Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 83

US-09-814-353-10775/c

/ Sequence 10775, Application US/09814353

/ Publication No. US20030165831A1

/ GENERAL INFORMATION:

/ APPLICANT: Lee, John

/ APPLICANT: Thompson, Pamela

/ APPLICANT: Lillie, James

/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

/ TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

/ FILE REFERENCE: MRI-006B

/ CURRENT APPLICATION NUMBER: US/09/814,353

/ CURRENT FILING DATE: 2001-03-21

/ PRIOR APPLICATION NUMBER: US 60/191,031

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; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10775
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 31, 98, 159, 166, 289, 348, 361, 364, 385, 393, 398, 400,
; LOCATION: 403, 410, 414, 419, 432, 457, 467
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-10775

Query Match 1.4%; Score 24; DB 3; Length 486;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 84
US-09-814-353-16367/c
; Sequence 16367, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16367
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 221
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-16367

Query Match 1.4%; Score 24; DB 3; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.13;
```

```
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 85 TAAGTACCTCGCGCGGACACGC 62

RESULT 85
US-09-814-353-15976/c
; Sequence 15976, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TYPE: DNA
; ORGANISM: Homo sapiens
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15976
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-15976

Query Match 1.4%; Score 24; DB 3; Length 517;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 102 TAAGTACCTCGCGCGGACACGC 79

RESULT 86
US-09-814-353-4993/c
; Sequence 4993, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TYPE: DNA
; ORGANISM: Homo sapiens
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
```

```
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4993
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 443, 491
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4993
```

```
Query Match 1.4%; Score 24; DB 3; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1690 TAAGTACCTCGGCGGACCAAGC 1713
|||||
Db 30 TAAGTACCTCGGCGGACCAAGC 7
```

RESULT 87

```
US-09-814-353-11286/c
; Sequence 11286, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11286
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 443, 491
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-11286
```

```
Query Match 1.4%; Score 24; DB 3; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1690 TAAGTACCTCGGCGGACCAAGC 1713
|||||
Db 30 TAAGTACCTCGGCGGACCAAGC 7
```

RESULT 88

```
US-09-814-353-15615/c
```

```
; Sequence 15615, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15615
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-15615
```

```
Query Match 1.4%; Score 24; DB 3; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1690 TAAGTACCTCGGCGGACCAAGC 1713
|||||
Db 106 TAAGTACCTCGGCGGACCAAGC 83
```

RESULT 89

```
US-09-814-353-17892/c
; Sequence 17892, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17892
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 350
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-17892

Query Match      1.4%; Score 24; DB 3; Length 524;
Best Local Similarity 100.0%; Pred.No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690 TAAGTACTCGCGCGACACG 1713
      |||||
Db      109 TAAGTACTCGCGCGACACG 86

RESULT 90
US-09-814-353-5823/c
; Sequence 5823, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5823
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 435
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-5823

Query Match      1.4%; Score 24; DB 3; Length 534;
Best Local Similarity 100.0%; Pred.No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690 TAAGTACTCGCGCGACACG 1713
      |||||
Db      30 TAAGTACTCGCGCGACACG 7

RESULT 91
US-09-814-353-12105/c
; Sequence 12105, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

```

```
Query Match
Best Local Similarity 1.4%; Score 24; DB 3; Length 546;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 105 TAAGTACCTCGGCGGACACGC 82

RESULT 93
US-09-814-353-6042/c
; Sequence 6042, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6042
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapiens
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6042
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapiens
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6042
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapiens
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39396
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-357-930-39396

Query Match
Best Local Similarity 1.4%; Score 24; DB 3; Length 548;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 30 TAAGTACCTCGGCGGACACGC 7

RESULT 94
US-09-814-353-12321/c
; Sequence 12321, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39396
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-357-930-39396

Query Match
Best Local Similarity 1.4%; Score 24; DB 8; Length 569;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 30 TAAGTACCTCGGCGGACACGC 7
```

```
Query Match
Best Local Similarity 1.4%; Score 24; DB 3; Length 548;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 30 TAAGTACCTCGGCGGACACGC 7

RESULT 95
US-10-357-930-39396/c
; Sequence 39396, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39396
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-357-930-39396

Query Match
Best Local Similarity 1.4%; Score 24; DB 8; Length 569;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 30 TAAGTACCTCGGCGGACACGC 7
```

```
Db      85  TAAGTACCTCGCGCGGACCAACGC 62

RESULT 96
US-10-357-930-43996/c
; Sequence 43996, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43996
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-43996

Query Match      1.4%; Score 24; DB 8; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690  TAAGTACCTCGCGCGGACCAACGC 1713
Db      85  TAAGTACCTCGCGCGGACCAACGC 62

RESULT 97
US-09-814-353-18489/c
; Sequence 18489, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672

US-09-814-353-18489

Query Match      1.4%; Score 24; DB 8; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690  TAAGTACCTCGCGCGGACCAACGC 1713
Db      351  TAAGTACCTCGCGCGGACCAACGC 374

RESULT 98
US-10-357-930-36049
; Sequence 36049, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36049
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-36049

Query Match      1.4%; Score 24; DB 8; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690  TAAGTACCTCGCGCGGACCAACGC 1713
Db      351  TAAGTACCTCGCGCGGACCAACGC 374

RESULT 99
US-10-357-930-45110
; Sequence 45110, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
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; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4510
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-45110

Query Match 1.4%; Score 24; DB 8; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 100
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; Sequence 112, Application US/10950009
; Publication No. US2005006934A1
; GENERAL INFORMATION:
; APPLICANT: BERKA, Randy
; APPLICANT: BASHKIROVA, Elena
; APPLICANT: REV, Michael
; TITLE OF INVENTION: Methods For Monitoring Gene Expression
; FILE REFERENCE: 10541.200-US
; CURRENT APPLICATION NUMBER: US/10/950,009
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: 60/506,140
; PRIOR FILING DATE: 2003-09-25
; NUMBER OF SEQ ID NOS: 1190
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Trichoderma reesei
US-10-950-009-112

Query Match 1.4%; Score 24; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACCCACGC 1713
DB 24 TAAGTACCTCGCGCGACCCACGC 1

Search completed: March 11, 2006, 22:31:51
Job time : 1455 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 21:01:03 ; Search time 679 Seconds
(without alignments)

5820.912 Million cell updates/sec

Title: US-09-989-890-105

Perfect score: 1713

Sequence: 1 atgcccgcctggacaccc.....tacctggcgcgaccacgc 1713

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 7673375 seqs, 1153648444 residues

Word size: 0

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Published Applications NA_New.*

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- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
- 11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
- 12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1594	93.1	1785	9	US-11-072-512-799
2	25	1.5	25	8	US-10-310-914A-1045304
3	25	1.5	25	8	US-10-310-914A-1045320
4	25	1.5	25	12	US-11-121-849-344330
5	25	1.5	25	12	US-11-121-849-344331
6	25	1.5	25	12	US-11-121-849-344332
7	25	1.5	25	12	US-11-121-849-344333
8	25	1.5	25	12	US-11-121-849-344334
9	25	1.5	25	12	US-11-121-849-344335
10	25	1.5	25	12	US-11-121-849-344336
11	25	1.5	25	12	US-11-121-849-344337
12	25	1.5	25	12	US-11-121-849-344338
13	25	1.5	25	12	US-11-121-849-344339
14	25	1.5	25	12	US-11-121-849-344340
15	25	1.5	25	12	US-11-121-849-344517
16	25	1.5	25	12	US-11-121-849-344518
17	25	1.5	25	12	US-11-121-849-344519
18	25	1.5	25	12	US-11-121-849-344520
19	25	1.5	25	12	US-11-121-849-344521
20	25	1.5	25	12	US-11-121-849-344522

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22	25	1.5	25	12	US-11-121-849-344524	Sequence 344524,
23	25	1.5	25	12	US-11-121-849-344525	Sequence 344525,
24	25	1.5	25	12	US-11-121-849-344526	Sequence 344526,
25	25	1.5	25	12	US-11-121-849-344527	Sequence 344527,
26	24	1.4	24	8	US-10-310-914A-1045318	Sequence 1045318,
27	24	1.4	24	8	US-10-310-914A-1045328	Sequence 1045328,
28	23	1.3	23	8	US-10-310-914A-1045311	Sequence 1045311,
29	23	1.3	23	8	US-10-310-914A-1045322	Sequence 1045322,
30	23	1.3	23	8	US-10-310-914A-1045327	Sequence 1045327,
31	23	1.3	23	8	US-10-310-914A-1045337	Sequence 1045337,
32	22	1.3	22	8	US-10-310-914A-1045303	Sequence 1045303,
33	22	1.3	22	8	US-10-310-914A-1045306	Sequence 1045306,
34	22	1.3	22	8	US-10-310-914A-1045307	Sequence 1045307,
35	22	1.3	22	8	US-10-310-914A-1045309	Sequence 1045309,
36	22	1.3	22	8	US-10-310-914A-1045310	Sequence 1045310,
37	22	1.3	22	8	US-10-310-914A-1045313	Sequence 1045313,
38	22	1.3	22	8	US-10-310-914A-1045314	Sequence 1045314,
39	22	1.3	22	8	US-10-310-914A-1045315	Sequence 1045315,
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41	22	1.3	22	8	US-10-310-914A-1045323	Sequence 1045323,
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44	22	1.3	22	8	US-10-310-914A-1045330	Sequence 1045330,
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46	21	1.2	21	8	US-10-310-914A-1045305	Sequence 1045305,
47	21	1.2	21	8	US-10-310-914A-1045303	Sequence 1045303,
48	21	1.2	301	12	US-11-234-786-293	Sequence 293, App
49	21	1.2	305	9	US-11-116-881A-2005	Sequence 2005, App
50	21	1.2	405	9	US-11-116-881A-992	Sequence 992, App
51	21	1.2	509	9	US-11-057-484A-13	Sequence 13, Appl
52	21	1.2	582	12	US-11-201-194-5	Sequence 5, Appl
53	21	1.2	1820	9	US-11-206-587-4	Sequence 4, Appl
54	20	1.2	20	8	US-10-310-914A-1045308	Sequence 1045308,
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56	20	1.2	25	12	US-11-136-527-193835	Sequence 193835,
57	20	1.2	25	12	US-11-136-527-193843	Sequence 193843,
58	20	1.2	25	12	US-11-136-527-193849	Sequence 193849,
59	20	1.2	25	12	US-11-136-527-193854	Sequence 193854,
60	20	1.2	43	12	US-11-031-356-14	Sequence 14, Appl
61	20	1.2	486	6	US-09-925-065A-613855	Sequence 613855,
62	20	1.2	680	12	US-11-136-527-3780	Sequence 3780, App
63	20	1.2	680	12	US-11-136-527-7876	Sequence 7876, App
64	20	1.2	993	8	US-10-750-185-36767	Sequence 36767, A
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66	20	1.2	1280	9	US-11-096-568A-25683	Sequence 25683, A
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141	19	1.1	19	10	US-11-101-244-1430826	Sequence 1430826,	Sequence 1430826,	215	19	1.1	19	11	US-11-083-784-1430827	Sequence 1430827,
142	19	1.1	19	10	US-11-101-244-1430827	Sequence 1430827,	Sequence 1430827,	216	19	1.1	19	11	US-11-083-784-1430828	Sequence 1430828,
143	19	1.1	19	10	US-11-101-244-1430828	Sequence 1430828,	Sequence 1430828,	215	19	1.1	19	11	US-11-031-356-11	Sequence 11, Appl
144	19	1.1	19	11	US-11-083-784-1430754	Sequence 1430754,	Sequence 1430754,	215	19	1.1	20	12	US-11-063-343-44	Sequence 44, Appl
145	19	1.1	19	11	US-11-083-784-1430755	Sequence 1430755,	Sequence 1430755,	216	19	1.1	20	12	US-11-136-527-193845	Sequence 193845,
146	19	1.1	19	11	US-11-083-784-1430756	Sequence 1430756,	Sequence 1430756,	218	19	1.1	42	12	US-11-063-343-41	Sequence 41, Appl
147	19	1.1	19	11	US-11-083-784-1430757	Sequence 1430757,	Sequence 1430757,	219	19	1.1	43	12	US-11-031-356-6	Sequence 6, Appl
148	19	1.1	19	11	US-11-083-784-1430758	Sequence 1430758,	Sequence 1430758,	220	19	1.1	170	12	US-11-108-172-57	Sequence 57, Appl
149	19	1.1	19	11	US-11-083-784-1430759	Sequence 1430759,	Sequence 1430759,	221	19	1.1	204	12	US-11-108-172-66	Sequence 66, Appl
150	19	1.1	19	11	US-11-083-784-1430760	Sequence 1430760,	Sequence 1430760,	222	19	1.1	300	12	US-11-234-786-297	Sequence 297, App
151	19	1.1	19	11	US-11-083-784-1430761	Sequence 1430761,	Sequence 1430761,	223	19	1.1	332	12	US-11-108-172-6	Sequence 6, Appl
152	19	1.1	19	11	US-11-083-784-1430762	Sequence 1430762,	Sequence 1430762,	224	19	1.1	340	12	US-11-108-172-60	Sequence 60, Appl
153	19	1.1	19	11	US-11-083-784-1430763	Sequence 1430763,	Sequence 1430763,	225	19	1.1	370	8	US-10-623-155-140	Sequence 140, App
154	19	1.1	19	11	US-11-083-784-1430764	Sequence 1430764,	Sequence 1430764,	226	19	1.1	371	8	US-10-623-155-139	Sequence 139, App
155	19	1.1	19	11	US-11-083-784-1430765	Sequence 1430765,	Sequence 1430765,	227	19	1.1	371	8	US-10-623-155-141	Sequence 141, App
156	19	1.1	19	11	US-11-083-784-1430766	Sequence 1430766,	Sequence 1430766,	228	19	1.1	371	8	US-10-623-155-145	Sequence 145, App
157	19	1.1	19	11	US-11-083-784-1430767	Sequence 1430767,	Sequence 1430767,	229	19	1.1	420	12	US-11-108-172-56	Sequence 56, Appl
158	19	1.1	19	11	US-11-083-784-1430768	Sequence 1430768,	Sequence 1430768,	230	19	1.1	431	12	US-11-108-172-622	Sequence 622, App
159	19	1.1	19	11	US-11-083-784-1430769	Sequence 1430769,	Sequence 1430769,	231	19	1.1	537	6	US-09-925-065A-814229	Sequence 814229,
160	19	1.1	19	11	US-11-083-784-1430770	Sequence 1430770,	Sequence 1430770,	232	19	1.1	594	6	US-09-925-065A-4047	Sequence 4047, Ap
161	19	1.1	19	11	US-11-083-784-1430771	Sequence 1430771,	Sequence 1430771,	233	19	1.1	607	6	US-09-925-065A-521103	Sequence 521103,
162	19	1.1	19	11	US-11-083-784-1430772	Sequence 1430772,	Sequence 1430772,	234	19	1.1	608	6	US-09-925-065A-881709	Sequence 881709,
163	19	1.1	19	11	US-11-083-784-1430773	Sequence 1430773,	Sequence 1430773,	235	19	1.1	619	6	US-09-925-065A-515849	Sequence 515849,
164	19	1.1	19	11	US-11-083-784-1430774	Sequence 1430774,	Sequence 1430774,	236	19	1.1	619	6	US-09-925-065A-515850	Sequence 515850,
165	19	1.1	19	11	US-11-083-784-1430775	Sequence 1430775,	Sequence 1430775,	237	19	1.1	620	6	US-09-925-065A-844796	Sequence 844796,
166	19	1.1	19	11	US-11-083-784-1430776	Sequence 1430776,	Sequence 1430776,	238	19	1.1	623	6	US-09-925-065A-884608	Sequence 884608,
	19	1.1	19	11	US-11-083-784-1430777	Sequence 1430777,	Sequence 1430777,	239	19	1.1	623	6	US-09-925-065A-910579	Sequence 910579,

C 240	19	1.1	639	6	US-09-925-065A-517828	Sequence 517828,	C 313	18	1.1	86764	7	US-10-330-773-600	Sequence 600, App
C 241	19	1.1	936	8	US-10-750-185-36256	Sequence 36256, A	C 314	18	1.1	114801	12	US-11-121-086-22	Sequence 22, Appl
C 242	19	1.1	936	8	US-10-750-623-36256	Sequence 36256, A	C 315	18	1.1	162537	12	US-11-121-086-59	Sequence 59, Appl
C 243	19	1.1	1524	8	US-10-750-185-58349	Sequence 58349, A	C 316	18	1.1	163162	12	US-11-121-086-66	Sequence 66, Appl
C 244	19	1.1	1524	8	US-10-750-623-58349	Sequence 58349, A	C 317	18	1.1	171732	12	US-11-121-086-98	Sequence 98, Appl
C 245	19	1.1	1739	12	US-11-112-908-363	Sequence 363, App	C 318	17	1.0	19	10	US-11-101-244-463615	Sequence 463615,
C 246	19	1.1	2799	6	US-09-925-065A-554137	Sequence 554137, A	C 319	17	1.0	19	11	US-11-083-784-463615	Sequence 815013,
C 247	19	1.1	3065	8	US-10-750-185-63119	Sequence 63119, A	C 320	17	1.0	20	8	US-10-310-914A-815013	Sequence 815013,
C 248	19	1.1	3065	8	US-10-750-623-63119	Sequence 63119, A	C 321	17	1.0	25	7	US-10-932-182A-54638	Sequence 54638, A
C 249	19	1.1	4364	9	US-11-245-147-172	Sequence 172, App	C 322	17	1.0	25	7	US-10-932-182A-54638	Sequence 54638, A
C 250	19	1.1	4364	9	US-11-245-147-233	Sequence 233, App	C 323	17	1.0	25	12	US-11-121-849-7454	Sequence 7454, Ap
C 251	19	1.1	6087	12	US-11-000-463-485	Sequence 485, App	C 324	17	1.0	25	12	US-11-121-849-398779	Sequence 398779
C 252	19	1.1	18930	8	US-10-995-561-13213	Sequence 13213, A	C 325	17	1.0	25	12	US-11-121-849-400152	Sequence 400152,
C 253	19	1.1	16194	12	US-11-112-908-57	Sequence 57, Appl	C 326	17	1.0	25	12	US-11-136-527-193853	Sequence 193853,
C 254	18	1.1	18	8	US-10-310-914A-1045316	Sequence 1045316,	C 327	17	1.0	40	7	US-10-753-195-26	Sequence 26, Appl
C 255	18	1.1	18	8	US-10-310-914A-1045317	Sequence 1045317,	C 328	17	1.0	40	7	US-10-989-767A-664	Sequence 664, App
C 256	18	1.1	18	8	US-10-310-914A-1045326	Sequence 1045326,	C 329	17	1.0	40	7	US-10-989-767A-664	Sequence 664, App
C 257	18	1.1	18	8	US-10-310-914A-1045336	Sequence 1045336,	C 330	17	1.0	40	8	US-10-859-643-755	Sequence 755, App
C 258	18	1.1	20	7	US-10-753-195-30	Sequence 30, Appl	C 331	17	1.0	40	12	US-11-097-864-755	Sequence 755, App
C 259	18	1.1	20	7	US-10-989-767A-668	Sequence 668, App	C 332	17	1.0	40	12	US-11-097-864-755	Sequence 755, App
C 260	18	1.1	20	8	US-10-859-643-759	Sequence 759, App	C 333	17	1.0	201	8	US-10-995-561-26900	Sequence 26900, A
C 261	18	1.1	20	12	US-11-097-864-759	Sequence 759, App	C 334	17	1.0	201	8	US-10-995-561-26900	Sequence 26900, A
C 262	18	1.1	20	12	US-11-097-912-759	Sequence 759, App	C 335	17	1.0	201	8	US-10-995-561-32420	Sequence 32420, A
C 263	18	1.1	25	12	US-11-136-527-193846	Sequence 193846,	C 336	17	1.0	201	8	US-10-995-561-32430	Sequence 32430, A
C 264	18	1.1	25	12	US-11-136-527-193867	Sequence 193867,	C 337	17	1.0	231	7	US-10-932-182A-3666	Sequence 3666, Ap
C 265	18	1.1	65	8	US-10-310-914A-12176	Sequence 12176, A	C 338	17	1.0	231	7	US-10-932-182A-3666	Sequence 3666, Ap
C 266	18	1.1	201	8	US-10-995-561-61967	Sequence 61967, A	C 339	17	1.0	368	12	US-11-000-688-229	Sequence 229, App
C 267	18	1.1	201	8	US-10-995-561-62068	Sequence 62068, A	C 340	17	1.0	382	6	US-09-925-065A-218980	Sequence 218980,
C 268	18	1.1	201	12	US-11-124-368A-3102	Sequence 3102, Ap	C 341	17	1.0	387	7	US-10-932-182A-79065	Sequence 79065, A
C 269	18	1.1	201	12	US-11-124-368A-4125	Sequence 4125, Ap	C 342	17	1.0	387	7	US-10-932-182A-79065	Sequence 79065, A
C 270	18	1.1	201	12	US-11-000-688-91	Sequence 91, Appl	C 343	17	1.0	407	6	US-09-925-065A-507912	Sequence 507912,
C 271	18	1.1	301	12	US-11-234-788-230	Sequence 230, App	C 344	17	1.0	428	6	US-09-925-065A-216303	Sequence 216303,
C 272	18	1.1	512	6	US-09-925-065A-8330825	Sequence 8330825,	C 345	17	1.0	437	6	US-09-925-065A-216304	Sequence 216304,
C 273	18	1.1	512	6	US-09-925-065A-8330825	Sequence 8330825,	C 346	17	1.0	444	12	US-11-000-688-1577	Sequence 1577, Ap
C 274	18	1.1	563	6	US-09-925-065A-353713	Sequence 353713,	C 347	17	1.0	458	6	US-09-925-065A-401869	Sequence 401869,
C 275	18	1.1	565	6	US-09-925-065A-741456	Sequence 741456,	C 348	17	1.0	458	6	US-09-925-065A-401870	Sequence 401870,
C 276	18	1.1	570	6	US-09-925-065A-350145	Sequence 350145,	C 349	17	1.0	458	6	US-09-925-065A-401871	Sequence 401871,
C 277	18	1.1	570	6	US-09-925-065A-738650	Sequence 738650,	C 350	17	1.0	472	12	US-11-108-172-94	Sequence 94, Appl
C 278	18	1.1	570	6	US-09-925-065A-738651	Sequence 738651,	C 351	17	1.0	479	6	US-09-925-065A-318342	Sequence 318342,
C 279	18	1.1	582	6	US-09-925-065A-134986	Sequence 134986,	C 352	17	1.0	502	6	US-09-925-065A-398434	Sequence 398434,
C 280	18	1.1	607	6	US-09-925-065A-513479	Sequence 513479,	C 353	17	1.0	503	6	US-09-925-065A-379105	Sequence 379105,
C 281	18	1.1	614	6	US-09-925-065A-374068	Sequence 374068,	C 354	17	1.0	504	6	US-09-925-065A-334102	Sequence 334102,
C 282	18	1.1	614	6	US-09-925-065A-646302	Sequence 646302,	C 355	17	1.0	508	6	US-09-925-065A-194110	Sequence 194110,
C 283	18	1.1	615	6	US-09-925-065A-375993	Sequence 375993,	C 356	17	1.0	512	12	US-11-108-172-88	Sequence 88, Appl
C 284	18	1.1	615	6	US-09-925-065A-375994	Sequence 375994,	C 357	17	1.0	517	6	US-09-925-065A-510849	Sequence 510849,
C 285	18	1.1	619	6	US-09-925-065A-385595	Sequence 385595,	C 358	17	1.0	520	6	US-09-925-065A-457399	Sequence 457399,
C 286	18	1.1	619	6	US-09-925-065A-385596	Sequence 385596,	C 359	17	1.0	529	6	US-09-925-065A-378664	Sequence 378664,
C 287	18	1.1	619	6	US-09-925-065A-385597	Sequence 385597,	C 360	17	1.0	529	6	US-09-925-065A-536447	Sequence 536447,
C 288	18	1.1	626	6	US-09-925-065A-385597	Sequence 385597,	C 361	17	1.0	529	6	US-09-925-065A-536448	Sequence 536448,
C 289	18	1.1	634	6	US-09-925-065A-814641	Sequence 814641,	C 362	17	1.0	533	6	US-09-925-065A-344194	Sequence 344194,
C 290	18	1.1	637	6	US-09-925-065A-814249	Sequence 814249,	C 363	17	1.0	538	6	US-09-925-065A-344195	Sequence 344195,
C 291	18	1.1	638	6	US-09-925-065A-826845	Sequence 826845,	C 364	17	1.0	538	6	US-09-925-065A-9956	Sequence 9956, Ap
C 292	18	1.1	638	6	US-09-925-065A-834468	Sequence 834468,	C 365	17	1.0	545	6	US-09-925-065A-624168	Sequence 624168,
C 293	18	1.1	639	6	US-09-925-065A-482417	Sequence 482417,	C 366	17	1.0	548	6	US-09-925-065A-52567	Sequence 52567, A
C 294	18	1.1	640	6	US-09-925-065A-826248	Sequence 826248,	C 367	17	1.0	548	6	US-09-925-065A-52567	Sequence 52567, A
C 295	18	1.1	656	6	US-09-925-065A-716809	Sequence 716809,	C 368	17	1.0	548	6	US-09-925-065A-181548	Sequence 181548,
C 296	18	1.1	661	6	US-09-925-065A-917118	Sequence 917118,	C 369	17	1.0	549	6	US-09-925-065A-476079	Sequence 476079,
C 297	18	1.1	777	7	US-10-932-182A-4384	Sequence 4384, Ap	C 370	17	1.0	549	6	US-09-925-065A-476080	Sequence 476080,
C 298	18	1.1	777	7	US-10-932-182A-4384	Sequence 4384, Ap	C 371	17	1.0	549	6	US-09-925-065A-476081	Sequence 476081,
C 299	18	1.1	845	12	US-11-150-888-22	Sequence 22, Appl	C 372	17	1.0	549	6	US-09-925-065A-476082	Sequence 476082,
C 300	18	1.1	1094	6	US-09-925-065A-720390	Sequence 720390,	C 373	17	1.0	549	6	US-09-925-065A-861215	Sequence 861215,
C 301	18	1.1	1303	8	US-10-750-185-42410	Sequence 42410, A	C 374	17	1.0	550	6	US-09-925-065A-934849	Sequence 934849,
C 302	18	1.1	1303	8	US-10-750-623-42410	Sequence 42410, A	C 375	17	1.0	551	6	US-09-925-065A-512767	Sequence 512767,
C 303	18	1.1	1548	8	US-10-775-169-178	Sequence 178, App	C 376	17	1.0	553	6	US-09-925-065A-389617	Sequence 389617,
C 304	18	1.1	1563	8	US-10-750-185-26090	Sequence 26090, A	C 377	17	1.0	553	6	US-09-925-065A-389618	Sequence 389618,
C 305	18	1.1	1563	8	US-10-750-623-26090	Sequence 26090, A	C 378	17	1.0	555	6	US-09-925-065A-90074	Sequence 90074, A
C 306	18	1.1	1814	8	US-10-750-185-51351	Sequence 51351, A	C 379	17	1.0	559	6	US-09-925-065A-480681	Sequence 480681,
C 307	18	1.1	1814	8	US-10-750-623-51351	Sequence 51351, A	C 380	17	1.0	559	6	US-09-925-065A-480682	Sequence 480682,
C 308	18	1.1	2454	9	US-11-072-512-275	Sequence 275, App	C 381	17	1.0	560	6	US-09-925-065A-942690	Sequence 942690,
C 309	18	1.1	2625	9	US-11-072-512-986	Sequence 986, App	C 382	17	1.0	562	6	US-09-925-065A-237859	Sequence 237859,
C 310	18	1.1	2845	6	US-09-925-065A-681694	Sequence 681694,	C 383	17	1.0	564	6	US-09-925-065A-451113	Sequence 451113,
C 311	18	1.1	3496	9	US-11-072-512-1039	Sequence 1039, Ap	C 384	17	1.0	574	6	US-09-925-065A-511080	Sequence 511080,
C 312	18	1.1	76437	12	US-11-124-367A-5041	Sequence 5041, Ap	C 385	17	1.0	574	6	US-09-925-065A-511081	Sequence 511081,

C 386	17	1.0	578	6	US-09-925-065A-227065	Sequence 227065,	17	1.0	686	6	US-09-925-065A-883910	Sequence 883910,
C 387	17	1.0	578	6	US-09-925-065A-353773	Sequence 353773,	17	1.0	690	6	US-09-925-065A-549864	Sequence 549864,
C 388	17	1.0	581	6	US-09-925-065A-467016	Sequence 467016,	17	1.0	695	8	US-10-750-185-62194	Sequence 62194, A
C 389	17	1.0	581	6	US-09-925-065A-467017	Sequence 467017,	17	1.0	695	8	US-10-750-623-62194	Sequence 62194, A
C 390	17	1.0	581	6	US-09-925-065A-496726	Sequence 496726,	17	1.0	699	6	US-09-925-065A-787901	Sequence 787901,
C 391	17	1.0	582	6	US-09-925-065A-93183	Sequence 93183, A	17	1.0	700	6	US-09-925-065A-920031	Sequence 920031,
C 392	17	1.0	583	6	US-09-925-065A-275934	Sequence 275934,	17	1.0	710	12	US-11-136-527-1607	Sequence 1607, Ap
C 393	17	1.0	587	6	US-09-925-065A-773249	Sequence 773249,	17	1.0	717	6	US-09-925-065A-920100	Sequence 920100,
C 394	17	1.0	588	6	US-09-925-065A-126992	Sequence 126992,	17	1.0	718	6	US-09-925-065A-919829	Sequence 919829,
C 395	17	1.0	588	6	US-09-925-065A-126993	Sequence 126993,	17	1.0	735	8	US-10-967-093-7	Sequence 7, Appli
C 396	17	1.0	588	6	US-09-925-065A-731161	Sequence 731161,	17	1.0	742	8	US-10-750-185-27304	Sequence 27304, A
C 397	17	1.0	588	6	US-09-925-065A-810905	Sequence 810905,	17	1.0	742	8	US-10-750-623-27304	Sequence 27304, A
C 398	17	1.0	591	6	US-09-925-065A-93646	Sequence 93646, A	17	1.0	797	6	US-09-925-065A-730477	Sequence 730477,
C 399	17	1.0	591	6	US-09-925-065A-93647	Sequence 93647, A	17	1.0	801	6	US-09-925-065A-918197	Sequence 918197,
C 400	17	1.0	591	6	US-09-925-065A-93648	Sequence 93648, A	17	1.0	801	8	US-10-750-185-56880	Sequence 56880, A
C 401	17	1.0	594	6	US-09-925-065A-400035	Sequence 400035,	17	1.0	801	8	US-10-750-623-56880	Sequence 56880, A
C 402	17	1.0	598	6	US-09-925-065A-303099	Sequence 303099,	17	1.0	838	6	US-09-925-065A-919345	Sequence 919345,
C 403	17	1.0	600	8	US-10-750-185-20043	Sequence 20043, A	17	1.0	841	6	US-09-925-065A-924260	Sequence 924260,
C 404	17	1.0	600	8	US-10-750-623-20043	Sequence 20043, A	17	1.0	841	6	US-09-925-065A-924261	Sequence 924261,
C 405	17	1.0	600	12	US-11-136-527-4791	Sequence 4791, Ap	17	1.0	841	6	US-09-925-065A-924262	Sequence 924262,
C 406	17	1.0	605	12	US-11-136-527-5703	Sequence 5703, Ap	17	1.0	879	12	US-11-055-822-133	Sequence 133, App
C 407	17	1.0	605	6	US-09-925-065A-73280	Sequence 73280, A	17	1.0	879	12	US-11-055-822-1119	Sequence 1119, Ap
C 408	17	1.0	605	6	US-09-925-065A-73281	Sequence 73281, A	17	1.0	917	6	US-09-925-065A-690458	Sequence 690458,
C 409	17	1.0	608	6	US-09-925-065A-380695	Sequence 380695,	17	1.0	1039	8	US-10-750-185-44119	Sequence 44119, A
C 410	17	1.0	608	6	US-09-925-065A-946601	Sequence 946601,	17	1.0	1039	8	US-10-750-623-44119	Sequence 44119, A
C 411	17	1.0	613	6	US-09-925-065A-376923	Sequence 376923,	17	1.0	1103	6	US-09-925-065A-70025	Sequence 70025, A
C 412	17	1.0	613	6	US-09-925-065A-376924	Sequence 376924,	17	1.0	1119	6	US-09-925-065A-715798	Sequence 715798,
C 413	17	1.0	613	6	US-09-925-065A-743906	Sequence 743906,	17	1.0	1172	8	US-10-750-185-37219	Sequence 37219, A
C 414	17	1.0	616	6	US-09-925-065A-395673	Sequence 395673,	17	1.0	1172	8	US-10-750-623-37219	Sequence 37219, A
C 415	17	1.0	618	6	US-09-925-065A-79914	Sequence 79914, A	17	1.0	1198	8	US-10-750-185-46309	Sequence 46309, A
C 416	17	1.0	619	6	US-09-925-065A-496993	Sequence 496993,	17	1.0	1198	8	US-10-750-623-46309	Sequence 46309, A
C 417	17	1.0	619	6	US-09-925-065A-496994	Sequence 496994,	17	1.0	1213	6	US-09-925-065A-23616	Sequence 23616, A
C 418	17	1.0	619	6	US-09-925-065A-496995	Sequence 496995,	17	1.0	1239	6	US-09-925-065A-65686	Sequence 65686, A
C 419	17	1.0	622	6	US-09-925-065A-53912	Sequence 53912, A	17	1.0	1239	6	US-09-925-065A-55687	Sequence 55687, A
C 420	17	1.0	625	6	US-09-925-065A-271065	Sequence 271065,	17	1.0	1239	6	US-09-925-065A-65688	Sequence 65688, A
C 421	17	1.0	625	6	US-09-925-065A-271066	Sequence 271066,	17	1.0	1244	6	US-09-925-065A-65689	Sequence 65689, A
C 422	17	1.0	625	6	US-09-925-065A-271067	Sequence 271067,	17	1.0	1244	6	US-09-925-065A-701443	Sequence 701443,
C 423	17	1.0	625	6	US-09-925-065A-271068	Sequence 271068,	17	1.0	1260	8	US-10-750-185-26652	Sequence 26652, A
C 424	17	1.0	628	6	US-09-925-065A-632812	Sequence 632812,	17	1.0	1260	8	US-10-750-623-26652	Sequence 26652, A
C 425	17	1.0	628	6	US-09-925-065A-632813	Sequence 632813,	17	1.0	1278	9	US-11-096-568A-5536	Sequence 5536, Ap
C 426	17	1.0	630	6	US-09-925-065A-509224	Sequence 509224,	17	1.0	1316	9	US-11-096-568A-5536	Sequence 5536, Ap
C 427	17	1.0	631	6	US-09-925-065A-54555	Sequence 54555, A	17	1.0	1316	9	US-11-096-568A-5536	Sequence 5536, Ap
C 428	17	1.0	631	6	US-09-925-065A-54556	Sequence 54556, A	17	1.0	1337	8	US-10-750-185-25170	Sequence 25170, A
C 429	17	1.0	631	9	US-11-051-720-353	Sequence 353, App						
C 430	17	1.0	631	9	US-11-051-720-1148	Sequence 1148, Ap						
C 431	17	1.0	633	6	US-09-925-065A-706232	Sequence 706232,						
C 432	17	1.0	633	6	US-09-925-065A-706233	Sequence 706233,						
C 433	17	1.0	633	6	US-09-925-065A-706234	Sequence 706234,						
C 434	17	1.0	635	6	US-09-925-065A-108915	Sequence 108915,						
C 435	17	1.0	637	6	US-09-925-065A-460705	Sequence 460705,						
C 436	17	1.0	637	6	US-09-925-065A-641864	Sequence 641864,						
C 437	17	1.0	637	6	US-09-925-065A-641865	Sequence 641865,						
C 438	17	1.0	641	6	US-09-925-065A-374485	Sequence 374485,						
C 439	17	1.0	641	6	US-09-925-065A-779232	Sequence 779232,						
C 440	17	1.0	643	6	US-09-925-065A-840577	Sequence 840577,						
C 441	17	1.0	643	6	US-09-925-065A-491856	Sequence 491856,						
C 442	17	1.0	644	6	US-09-925-065A-486613	Sequence 486613,						
C 443	17	1.0	645	6	US-09-925-065A-432050	Sequence 432050,						
C 444	17	1.0	645	6	US-09-925-065A-432051	Sequence 432051,						
C 445	17	1.0	646	6	US-09-925-065A-326016	Sequence 326016,						
C 446	17	1.0	646	6	US-09-925-065A-861292	Sequence 861292,						
C 447	17	1.0	649	6	US-09-925-065A-499607	Sequence 499607,						
C 448	17	1.0	649	6	US-09-925-065A-499608	Sequence 499608,						
C 449	17	1.0	649	6	US-09-925-065A-499609	Sequence 499609,						
C 450	17	1.0	649	6	US-09-925-065A-499610	Sequence 499610,						
C 451	17	1.0	665	6	US-09-925-065A-91060	Sequence 91060, A						
C 452	17	1.0	666	6	US-09-925-065A-880158	Sequence 880158,						
C 453	17	1.0	669	6	US-09-925-065A-515134	Sequence 515134,						
C 454	17	1.0	683	6	US-09-925-065A-73813	Sequence 73813, A						
C 455	17	1.0	685	6	US-09-925-065A-367620	Sequence 367620,						
C 456	17	1.0	685	6	US-09-925-065A-367621	Sequence 367621,						
C 457	17	1.0	685	6	US-09-925-065A-367622	Sequence 367622,						
C 458	17	1.0	686	6	US-09-925-065A-883909	Sequence 883909,						

ALIGNMENTS

RESULT 1

US-11-072-512-799
; Sequence 799, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HISO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512

CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 799
LENGTH: 1785
TYPE: DNA
ORGANISM: Homo sapiens
US-11-072-512-799

Query Match 93.1%; Score 1594; DB 9; Length 1785;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATCCCGCCCTGACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACCGTGGGAG 60
DB 90 ATCCCGCCCTGACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACCGTGGGAG 149

QY 61 CGGCCAACAGAGTATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCACGCGC 120
DB 150 CGGCCAACAGAGTATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCACGCGC 209

QY 121 CGCACCGGTAGACAGACCCCAAGGACCTGGGCCACATGGGCCAGAGACATTACTTC 180
DB 210 CGCACCGGTAGACAGACCCCAAGGACCTGGGCCACATGGGCCAGAGACATTACTTC 269

QY 181 ATCTCTGGCTCTGCTGAGCGCGGCTTGTAGTCTCCCGACCTGCTCTGGCGGACCC 240
DB 270 ATCTCTGGCTCTGCTGAGCGCGGCTTGTAGTCTCCCGACCTGCTCTGGCGGACCC 329

QY 241 TGGGTGTGGAGTGTGTGCGGGCTGCTTCTGCTCCGCGCTGCGGGATGCTCCAG 300
DB 330 TGGGTGTGGAGTGTGTGCGGGCTGCTTCTGCTCCGCGCTGCGGGATGCTCCAG 389

QY 301 CGCTGTGGAGCTGTGTGGGGATGCGGCCCTGCTGTCTACTGAGACCTCACTGAG 360
DB 390 CGCTGTGGAGCTGTGTGGGGATGCGGCCCTGCTGTCTACTGAGACCTCACTGAG 449

QY 361 GGGACTGCTGAAGCAACTGGGCCAAGGAGCAATGGAGTCCCGCCAGCCCTGATCGT 420
DB 450 GGGACTGCTGAAGCAACTGGGCCAAGGAGCAATGGAGTCCCGCCAGCCCTGATCGT 509

QY 421 GCACCCCGCCAGCGCGGGATGCGCGCTCAAGTCAACCATGGCGAGCAGCTTCAGC 480
DB 510 GCACCCCGCCAGCGCGGGATGCGCGCTCAAGTCAACCATGGCGAGCAGCTTCAGC 569

QY 481 TACCCCGATGTTAAGCTCAAGGATCCCTGTGTATCCCTACCCGAGGCGCACCTCCCA 540
DB 570 TACCCCGATGTTAAGCTCAAGGATCCCTGTGTATCCCTACCCGAGGCGCACCTCCCA 629

QY 541 GCGCTGTAGTCGAGCTCTGCTGCAAGGAGCCACTGGCGATCCCGCCACCCATGGACAC 600
DB 630 GCGCTGTAGTCGAGCTCTGCTGCAAGGAGCCACTGGCGATCCCGCCACCCATGGACAC 689

QY 601 AGCTGCGCCAGCACCTTTGCGAGTGTCTGCTGGCTCCGAGGAGTACTATTCTTCCAT 660
DB 690 AGCTGCGCCAGCACCTTTGCGAGTGTCTGCTGGCTCCGAGGAGTACTATTCTTCCAT 749

QY 661 GAGTCGGACCTGACCTGCGGAGATGGGAGTGGCTCCATGTCGAGCGGAGAAATGAT 720
DB 750 GAGTCGGACCTGACCTGCGGAGATGGGAGTGGCTCCATGTCGAGCGGAGAAATGAT 809

QY 721 GTGCTCATCTTCAAGAGCTGACAGCTGTTTACGCTACACAGATCGATGAGCTGGCC 780
DB 810 GTGCTCATCTTCAAGAGCTGACAGCTGTTTACGCTACACAGATCGATGAGCTGGCC 869

QY 781 AAGTGACATCAGACACTGTGTCTCGGAGAACAGCAGTAAGATCTCGACCTTATCAGC 840
DB 870 AAGTGACATCAGACACTGTGTCTCGGAGAACAGCAGTAAGATCTCGACCTTATCAGC 929

RESULT 2

US-10-310-914A-1045304/c
; Sequence 1045304, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06

QY 841 AGCATCAGCAGGACTACCACTGGATGACAGGATGCTGAGGGCGCCTGGTACGGGC 900
DB 930 AGCATCAGCAGGACTACCACTGGATGACAGGATGCTGAGGGCGCCTGGTACGGGC 989

QY 901 ATCAATTCGCAATTAGTACCCGAAAGAGCCGCTGCTCGCCACAGACCTCGGAGGGTCGTTCA 960
DB 990 ATCAATTCGCAATTAGTACCCGAAAGAGCCGCTGCTCGCCACAGACCTCGGAGGGTCGTTCA 1049

QY 961 ACTCGGGCTGTGCCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGC 1020
DB 1050 ACTCGGGCTGTGCCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGC 1109

QY 1021 TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGATGAGATGCC 1080
DB 1110 TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGATGAGATGCC 1169

QY 1081 ATGCCCGGAAAGCTGAGGCTTATGAGCTTCAGGGGTACCCAGCAAGCCATGATCATCC 1140
DB 1170 ATGCCCGGAAAGCTGAGGCTTATGAGCTTCAGGGGTACCCAGCAAGCCATGATCATCC 1229

QY 1141 TTCAGGGCACCGACACAGACTGCTCGGGGGACCCCTTGTCTCAGGTGTACTGCTAACCC 1200
DB 1230 TTCAGGGCACCGACACAGACTGCTCGGGGGACCCCTTGTCTCAGGTGTACTGCTAACCC 1289

QY 1201 CTGCCAGGCCAGCTGCCACACCCCTTCTTGGGAGAGCATGGCCTACAGAAATGAAGGG 1260
DB 1290 CTGCCAGGCCAGCTGCCACACCCCTTCTTGGGAGAGCATGGCCTACAGAAATGAAGGG 1349

QY 1261 GGACCAAGAAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGATGCCCACTCTGGCTCTCC 1320
DB 1350 GGACCAAGAAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGATGCCCACTCTGGCTCTCC 1409

QY 1321 TGCCTTGGCTGACTGGGTTCTTGGACCATGTGCAATTTCACTGGGCCATGGGATCTAATC 1380
DB 1410 TGCCTTGGCTGACTGGGTTCTTGGACCATGTGCAATTTCACTGGGCCATGGGATCTAATC 1469

QY 1381 TCTTGTGATCCCGAGTGTCTGATCCCTGCGAGGGCCCTTCTTCTGCTCATGGTCT 1440
DB 1470 TCTTGTGATCCCGAGTGTCTGATCCCTGCGAGGGCCCTTCTTCTGCTCATGGTCT 1529

QY 1441 TCAGGTGGCTCATCATGAAAGTAAAGGATGAGGATGAGCATTAACCTTCTGGGAGTGAACCTG 1500
DB 1530 TCAGGTGGCTCATCATGAAAGTAAAGGATGAGGATGAGCATTAACCTTCTGGGAGTGAACCTG 1589

QY 1501 ACTCCATCCCCCTATTGCCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAAT 1560
DB 1590 ACTCCATCCCCCTATTGCCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAAT 1649

QY 1561 TCACAGTTTAAAGAGCTTATCTTAATGATTTGTTGGGGGTGGGCGAGGGCCCACT 1620
DB 1650 TCACAGTTTAAAGAGCTTATCTTAATGATTTGTTGGGGGTGGGCGAGGGCCCACT 1709

QY 1621 CTATGTTATGTTAAGGAGTGTGTTCTGCTGATGTTCTGCTATCTTAAACATGAC 1680
DB 1710 CTATGTTATGTTAAGGAGTGTGTTCTGCTGATGTTCTGCTATCTTAAACATGAC 1769

QY 1681 CACAGTTTCTAAGTAC 1696
DB 1770 CACAGTTTCTAAGTAC 1785

; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045304
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045304

Query Match 1.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1475 GCATTACCTTCGGGAGTGAACCT 1499
Db 25 GCATTACCTTCGGGAGTGAACCT 1

RESULT 3

US-10-310-914A-1045320/c
; Sequence 1045320 Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045320
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045320

Query Match 1.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1382 CCTTGATCCCCAGCTGGTCTGATC 1406
Db 25 CCTTGATCCCCAGCTGGTCTGATC 1

RESULT 4

US-11-121-849-344330
; Sequence 344330, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344330
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344330

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1341 CTGGACCATGTGCATTTCTACTGGC 1365
|||||

Db 1 CTGGACCATGTGCATTTCTACTGGC 25

RESULT 5

US-11-121-849-344331
; Sequence 344331, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344331
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344331

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1356 TTCACTGGGCCATGGGATCTACATC 1380
Db 1 TTCACTGGGCCATGGGATCTACATC 25
|||||

RESULT 6

US-11-121-849-344332
; Sequence 344332, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344332
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344332

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1233 AGAAGCATGGCCTCAGCAATGAAGA 1257
Db 1 AGAAGCATGGCCTCAGCAATGAAGA 25
|||||

RESULT 7

US-11-121-849-344333
; Sequence 344333, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344333
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344333

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 CTGGCCATGGGATCTACATCTCT 1384
|||||
Db 1 CTGGCCATGGGATCTACATCTCT 25

RESULT 8

US-11-121-849-344334
; Sequence 344334, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344334
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344334

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 TGCTCATGCTTCAGGTGGCCTGA 1453
|||||
Db 1 TGCTCATGCTTCAGGTGGCCTGA 25

RESULT 9

US-11-121-849-344335
; Sequence 344335, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344335
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344335

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1466 AGGAGTTAGGCATTACCTTCTGGGA 1490
|||||
Db 1 AGGAGTTAGGCATTACCTTCTGGGA 25

RESULT 10

US-11-121-849-344336
; Sequence 344336, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344336
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344336

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 TACCTTCTGGGAGTGAACCTTGACT 1503
|||||
Db 1 TACCTTCTGGGAGTGAACCTTGACT 25

RESULT 11

US-11-121-849-344337
; Sequence 344337, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344337
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344337

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 ACCTTCTGGGAGTGAACCTTGACTC 1504
|||||
Db 1 ACCTTCTGGGAGTGAACCTTGACTC 25

RESULT 12

US-11-121-849-344338
; Sequence 344338, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma

```
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344338
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344338

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 GAACCCCTGTGGGAGAGGCTTAGAC 1292
Db 1 GAACCCCTGTGGGAGAGGCTTAGAC 25

RESULT 13
US-11-121-849-344339
; Sequence 344339, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344339
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344339

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1273 CCTGTGGGAGAGGCTTAGACCTGAA 1297
Db 1 CCTGTGGGAGAGGCTTAGACCTGAA 25

RESULT 14
US-11-121-849-344340
; Sequence 344340, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344340
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
```

```
US-11-121-849-344340

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1318 TCCTGCTTGGCTGACTGGGTTCCT 1342
Db 1 TCCTGCTTGGCTGACTGGGTTCCT 25

RESULT 15
US-11-121-849-344517
; Sequence 344517, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344517
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344517

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1356 TTCACCTGGGCCCATGGGATCTACATC 1380
Db 1 TTCACCTGGGCCCATGGGATCTACATC 25

RESULT 16
US-11-121-849-344518
; Sequence 344518, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344518
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344518

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1357 TCACTGGGCCCATGGGATCTACATCT 1381
Db 1 TCACTGGGCCCATGGGATCTACATCT 25

RESULT 17
US-11-121-849-344519
```

```
; Sequence 344519, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344519
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344519

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1359 ACTGGCCATGGGATCTACATCTCC 1383
Db 1 ACTGGCCATGGGATCTACATCTCC 25

RESULT 18
US-11-121-849-344520
; Sequence 344520, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344520
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344520

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1359 ACTGGCCATGGGATCTACATCTCC 1383
Db 1 ACTGGCCATGGGATCTACATCTCC 25

RESULT 19
US-11-121-849-344521
; Sequence 344521, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344521
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344521

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 CTGGCCATGGGATCTACATCTCT 1384
Db 1 CTGGCCATGGGATCTACATCTCT 25
```

```
; SEQ ID NO 344521
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344521

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1464 TAAGGAGTTAGGCATTACCTTCTGG 1488
Db 1 TAAGGAGTTAGGCATTACCTTCTGG 25

RESULT 20
US-11-121-849-344522
; Sequence 344522, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344522
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344522

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1466 AGGAGTTAGGCATTACCTTCTGGGA 1490
Db 1 AGGAGTTAGGCATTACCTTCTGGGA 25

RESULT 21
US-11-121-849-344523
; Sequence 344523, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344523
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344523

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1467 GGAGTTAGGCATTACCTTCTGGGAG 1491
Db 1 GGAGTTAGGCATTACCTTCTGGGAG 25
```



```
RESULT 22
US-11-121-849-344524
; Sequence 344524, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344524
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344524

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 TACCTTCTGGGAGTGAACCTGACT 1503
      |||||||||||||||||||||||||
Db 1 TACCTTCTGGGAGTGAACCTGACT 25

RESULT 23
US-11-121-849-344525
; Sequence 344525, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344525
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344525

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 ACCTTCTGGGAGTGAACCTGACTC 1504
      |||||||||||||||||||||||||
Db 1 ACCTTCTGGGAGTGAACCTGACTC 25

RESULT 24
US-11-121-849-344526
; Sequence 344526, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
```

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; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344526
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344526

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 GAACCCCTGTGGGAGGCTTAGAC 1292
      |||||||||||||||||||||||||
Db 1 GAACCCCTGTGGGAGGCTTAGAC 25

RESULT 25
US-11-121-849-344527
; Sequence 344527, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344527
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344527

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1273 CCTGTGGGAGGCTTAGACCTGAA 1297
      |||||||||||||||||||||||||
Db 1 CCTGTGGGAGGCTTAGACCTGAA 25

RESULT 26
US-10-310-914A-1045318/c
; Sequence 1045318, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045318
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045318

Query Match      1.4%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1378 ATCTCCTTCATCCCGAGCTGGTC 1401
|||||
Db 24 ATCTCCTTCATCCCGAGCTGGTC 1

RESULT 27
US-10-310-914A-1045328/c
; Sequence 1045328, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045328
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045328

Query Match 1.4%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1600 GGGGGTGGGCGAGGCCACTCTA 1623
|||||
Db 24 GGGGGTGGGCGAGGCCACTCTA 1

RESULT 28
US-10-310-914A-1045311/c
; Sequence 1045311, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045311
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045311

Query Match 1.3%; Score 23; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1436 GGTCTTCAGGTGGCTGATCATG 1458
|||||
Db 23 GGTCTTCAGGTGGCTGATCATG 1

RESULT 29
US-10-310-914A-1045322/c
; Sequence 1045322, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045322
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045322

Query Match 1.3%; Score 23; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1436 GGTCTTCAGGTGGCTGATCATG 1458
|||||
Db 23 GGTCTTCAGGTGGCTGATCATG 1

; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045322
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045322

Query Match 1.3%; Score 23; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1593 TTGTATTGGGGTGGCGAGGC 1615
|||||
Db 23 TTGTATTGGGGTGGCGAGGC 1

RESULT 30
US-10-310-914A-1045327/c
; Sequence 1045327, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045327
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045327

Query Match 1.3%; Score 23; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1267 GGAACCCCTGTGGAGAGGCTTA 1289
|||||
Db 23 GGAACCCCTGTGGAGAGGCTTA 1

RESULT 31
US-10-310-914A-1045337/c
; Sequence 1045337, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045337
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045337

Query Match 1.3%; Score 23; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1275 TGTGGGAGAGGCTTAGACCTGAA 1297

```
Db      23  TTGGGAGAGGCTTAGACCTGA 1
|||||
RESULT 32
US-10-310-914A-1045303/c
; Sequence 1045303, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045303
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045303

Query Match      1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1411 CCAGGGCCCTTCCTTCCTGCT 1432
|||||
Db      22  CCAGGGCCCTTCCTTCCTGCT 1

RESULT 33
US-10-310-914A-1045306/c
; Sequence 1045306, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045306
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045306

Query Match      1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1639 TTGGTCTCGTTCTTGCTGAT 1660
|||||
Db      22  TTGGTCTCGTTCTTGCTGAT 1

RESULT 34
US-10-310-914A-1045307/c
; Sequence 1045307, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
```

```
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045307
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045307

Query Match      1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1291 ACCTGAAGCAGTCCCACTCTG 1312
|||||
Db      22  ACCTGAAGCAGTCCCACTCTG 1

RESULT 35
US-10-310-914A-1045309/c
; Sequence 1045309, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045309
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045309

Query Match      1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1431 CTCATGCTCTTCAGTGGCTG 1452
|||||
Db      22  CTCATGCTCTTCAGTGGCTG 1

RESULT 36
US-10-310-914A-1045310/c
; Sequence 1045310, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045310
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045310

Query Match      1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1274 CTGTGGAGAGGCTTAGACCTG 1295
|||||
```

Db 22 CTGTGGGAGAGGCTTACACCTG 1

RESULT 37

US-10-310-914A-1045313/c
; Sequence 1045313, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045313
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045313

Query Match 1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1468 GAGTAGGCATTACCTTCTGGG 1489

Db 22 GAGTAGGCATTACCTTCTGGG 1

RESULT 38

US-10-310-914A-1045314/c
; Sequence 1045314, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045314
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045314

Query Match 1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1343 GGACCATGTGCATTTCACTGGG 1364

Db 22 GGACCATGTGCATTTCACTGGG 1

RESULT 39

US-10-310-914A-1045315/c
; Sequence 1045315, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045315
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045315

Query Match 1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1593 TTGTATTGGGGGTGGCAGGG 1614

Db 22 TTGTATTGGGGGTGGCAGGG 1

RESULT 40

US-10-310-914A-1045319/c
; Sequence 1045319, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045319
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045319

Query Match 1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1412 CAGGGCCCTTCCTTCCTGCTC 1433

Db 22 CAGGGCCCTTCCTTCCTGCTC 1

RESULT 41

US-10-310-914A-1045323/c
; Sequence 1045323, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045323
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045323

Query Match 1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1407 CCTGCCAGGGCCCTTCCTTCC 1428

Db 22 CCTGCCAGGGCCCTTCCTTCC 1

```
RESULT 42
US-10-310-914A-1045324/c
; Sequence 1045324, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045324
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045324
Query Match 1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1362 GGGCCATGGGACTACATCTCC 1383
Db 22 GGGCCATGGGACTACATCTCC 1

RESULT 43
US-10-310-914A-1045329/c
; Sequence 1045329, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045329
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045329
Query Match 1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1439 CTTCCAGTGGCCTGATCATGGA 1460
Db 22 CTTCCAGTGGCCTGATCATGGA 1

RESULT 44
US-10-310-914A-1045330/c
; Sequence 1045330, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
```

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045330
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045330
Query Match 1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1212 AGCTGCCACACCCCTTCTCGGA 1233
Db 22 AGCTGCCACACCCCTTCTCGGA 1

RESULT 45
US-10-310-914A-1045332/c
; Sequence 1045332, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045332
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045332
Query Match 1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1392 CCAGCTGGTCTGATCCCTGCCA 1413
Db 22 CCAGCTGGTCTGATCCCTGCCA 1

RESULT 46
US-10-310-914A-1045305/c
; Sequence 1045305, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045305
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045305
Query Match 1.2%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1604 GGTGGCAGGCGCCACTCTAT 1624
Db 21 GGTGGCAGGCGCCACTCTAT 1
```

RESULT 47

US-10-310-914A-1045333/c
; Sequence 1045333, Application US/10310914A
; Publication No. US20060003222A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045333
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045333

Query Match 1.2%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1509 CCCTATTGCGACCTTAACCA 1529
|||
DB 21 CCCTATTGCGACCTTAACCA 1

RESULT 48

US-11-234-786-293
; Sequence 293, Application US/11234786
; Publication No. US20060024301A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; TITLE OF INVENTION: POLYPEPTIDES THEREOF
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234.786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453

; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-234-786-293

Query Match 1.2%; Score 21; DB 12; Length 301;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGCGCGACCAACGC 1713
|||
DB 232 GTACCTCGCGCGACCAACGC 252

RESULT 49

US-11-116-881A-2005
; Sequence 2005, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116.881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2005
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-11-116-881A-2005

Query Match 1.2%; Score 21; DB 9; Length 305;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGCGCGACCAACGC 1713
|||
DB 283 GTACCTCGCGCGACCAACGC 303

RESULT 50

US-11-116-881A-992
; Sequence 992, Application US/11116881A

Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 992
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-11-116-881A-992

Query Match 1.2%; Score 21; DB 9; Length 405;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGGCGGACACGCG 1713
Db 283 GTACCTCGGCGGACACGCG 303

RESULT 51
US-11-057-484A-13/c
; Sequence 13, Application US/11057484A
; Publication No. US20060029931A1
; GENERAL INFORMATION:
; APPLICANT: Finkel, Terri H.
; APPLICANT: Yin, JiYi
; TITLE OF INVENTION: Cellular Genes Regulated by HIV-1
; TITLE OF INVENTION: Infection and Methods of Use Thereof
; FILE REFERENCE: CHOP 0146CIP
; CURRENT APPLICATION NUMBER: US/11/057,484A
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 10/368,803
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/358,495
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-057-484A-13

Query Match 1.2%; Score 21; DB 9; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGGCGGACACGCG 1713
Db 24 GTACCTCGGCGGACACGCG 4

RESULT 52

US-11-201-194-5
; Sequence 5, Application US/11201194
; Publication No. US20060019306A1
; GENERAL INFORMATION:
; APPLICANT: University College Cork - National University of Ireland,
; APPLICANT: Cork
; TITLE OF INVENTION: Detection of ochratoxin A producing fungi
; FILE REFERENCE: NATI25
; CURRENT APPLICATION NUMBER: US/11/201,194
; CURRENT FILING DATE: 2005-08-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Aspergillus ochraceus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (37)..(37)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (40)..(41)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (73)..(73)
; OTHER INFORMATION: n is a, c, g, or t
US-11-201-194-5

Query Match 1.2%; Score 21; DB 12; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGGCGGACACGCG 1713
Db 545 GTACCTCGGCGGACACGCG 565

RESULT 53

US-11-206-587-4/c
; Sequence 4, Application US/11206587
; Publication No. US20060040306A1
; GENERAL INFORMATION:
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
; TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 381552004900
; CURRENT APPLICATION NUMBER: US/11/206,587
; CURRENT FILING DATE: 2005-08-18
; PRIOR APPLICATION NUMBER: US/10/012,140
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: 60/246,768
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,772
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,185
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1820
; TYPE: DNA

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (146)...(1390)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1820)
; OTHER INFORMATION: n = A,T,C or G
US-11-206-587-4

Query Match
Best Local Similarity 100.0%; Score 21; DB 9; Length 1820;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACTCGCGCGGACACGC 1713
DB 27 GTACTCGCGCGGACACGC 7

RESULT 54
US-10-310-914A-1045308/c
; Sequence 1045308, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045308
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045308

Query Match
Best Local Similarity 100.0%; Score 20; DB 8; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 GCCACTCTGGCTCTCTCTG 1322
DB 20 GCCACTCTGGCTCTCTCTG 1

RESULT 55
US-10-310-914A-1045312/c
; Sequence 1045312, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045312
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045312

Query Match
Best Local Similarity 100.0%; Score 20; DB 8; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1418 CCTTCCTCTCTCTCTCTG 1437
```

```
DB 20 CCTTCCTCTCTCTCTCTG 1

RESULT 56
US-11-136-527-193835/c
; Sequence 193835, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193835
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-193835

Query Match
Best Local Similarity 100.0%; Score 20; DB 12; Length 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCTCTCTGCAAGGAG 570
DB 24 CGGACTCTCTCTGCAAGGAG 5

RESULT 57
US-11-136-527-193843/c
; Sequence 193843, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193843
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-193843

Query Match
Best Local Similarity 100.0%; Score 20; DB 12; Length 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCTCTCTGCAAGGAG 570
DB 20 CGGACTCTCTCTGCAAGGAG 1

RESULT 58
US-11-136-527-193849/c
; Sequence 193849, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
```



```
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193849
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-193849

Query Match          1.2%; Score 20; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCCTGCTGCAAGGAG 570
Db 21 CGGACTCCTGCTGCAAGGAG 2

RESULT 59
US-11-136-527-193854/c
; Sequence 193854, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193854
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-193854

Query Match          1.2%; Score 20; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCCTGCTGCAAGGAG 570
Db 23 CGGACTCCTGCTGCAAGGAG 4

RESULT 60
US-11-031-356-14/c
; Sequence 14, Application US/11031356
; Publication No. US20050272056A1
; GENERAL INFORMATION:
; APPLICANT: Quark Biotech Inc.
; APPLICANT: Deiss et al., Louis. P.
; TITLE OF INVENTION: Gene Identification Method
; FILE REFERENCE: 65507-F / 003/PCT1-US4
; CURRENT APPLICATION NUMBER: US/11/031,356
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 10/704,112
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 09/499,553
```

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; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/284,782
; PRIOR FILING DATE: 1993-07-06
; PRIOR APPLICATION NUMBER: 6,057,111
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: PCT/US97/20989
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/030,549
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Primer
US-11-031-356-14

Query Match          1.2%; Score 20; DB 12; Length 43;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1694 TACCTCGCGCGGACCACGC 1713
Db 43 TACCTCGCGCGGACCACGC 24

RESULT 61
US-09-925-065A-613855/c
; Sequence 613855, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 613855
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 481, 482, 483, 484, 485, 486
; OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-613855

Query Match          1.2%; Score 20; DB 6; Length 486;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1101 TTATGGAGCTCCAGGGTACC 1120
Db 251 TTATGGAGCTCCAGGGTACC 232

RESULT 62
US-11-136-527-3780/c
; Sequence 3780, Application US/11136527
```

```
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3780
; LENGTH: 680
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-7870

Query Match      1.2%; Score 20; DB 12; Length 680;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCCTCTGCTCAAGGAG 570
DB 238 CGGACTCCTCTGCTCAAGGAG 219

RESULT 63
US-11-136-527-7876/c
; Sequence 7876, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7876
; LENGTH: 680
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-7876

Query Match      1.2%; Score 20; DB 12; Length 680;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCCTCTGCTCAAGGAG 570
DB 238 CGGACTCCTCTGCTCAAGGAG 219

RESULT 64
US-10-750-185-36767/c
; Sequence 36767, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
```

```
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36767
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Bovine 19866880507628
US-10-750-185-36767

Query Match      1.2%; Score 20; DB 8; Length 993;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1312 GGCTCCTCTGCTTGGCTG 1331
DB 892 GGCTCCTCTGCTTGGCTG 873

RESULT 65
US-10-750-623-36767/c
; Sequence 36767, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36767
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Bovine 19866880507628
US-10-750-623-36767

Query Match      1.2%; Score 20; DB 8; Length 993;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1312 GGCTCCTCTGCTTGGCTG 1331
DB 892 GGCTCCTCTGCTTGGCTG 873

RESULT 66
US-11-096-568A-25683/c
; Sequence 25683, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25683
; LENGTH: 1280
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1280)
```

; OTHER INFORMATION: Ceres Seq. ID no. 13492847
US-11-096-568A-25683

Query Match 1.2%; Score 20; DB 9; Length 1280;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GGCAGCAGCTTCAGTACCC 485
|||||
DB 510 GGCAGCAGCTTCAGTACCC 491

RESULT 67

US-11-136-527-3889
; Sequence 3889, Application US/11136527
; Publication No. US20050287570A1

; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294

; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3889

; LENGTH: 13894

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-11-136-527-3889

Query Match 1.2%; Score 20; DB 12; Length 13894;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCCTGCTGCAAGGAG 570
|||||
DB 3394 CGGACTCCTGCTGCAAGGAG 3413

RESULT 68

US-10-310-914A-1045321/c
; Sequence 1045321, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087-0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1045321

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1045321

Query Match 1.1%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1225 TTCTGGGAGAGCATGGC 1243
|||||
DB 19 TTCTGGGAGAGCATGGC 1

RESULT 69

US-10-310-914A-1045325/c

; Sequence 1045325, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087-0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1045325

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1045325

Query Match 1.1%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 ACCTTCTGGAGTGAACCC 1498
|||||
DB 19 ACCTTCTGGAGTGAACCC 1

RESULT 70

US-10-310-914A-1045331/c

; Sequence 1045331, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087-0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1045331

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1045331

Query Match 1.1%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1201 CTGCCAGGCCAGCTGCCA 1219
|||||
DB 19 CTGCCAGGCCAGCTGCCA 1

RESULT 71

US-10-310-914A-1045334/c

; Sequence 1045334, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087-0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1045334

; LENGTH: 19

; TYPE: RNA

```
; ORGANISM: Human
US-10-310-914A-1045334

Query Match      1.1%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1203 GCCAGGCCAGCTGCCACA 1221
DB 19 GCCAGGCCAGCTGCCACA 1

RESULT 72
US-10-310-914A-1045335/c
; Sequence 1045335, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1045335
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045335

Query Match      1.1%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1203 GCCAGGCCAGCTGCCACA 1221
DB 19 GCCAGGCCAGCTGCCACA 1

RESULT 73
US-11-101-244-1430754
; Sequence 1430754, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430754
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430754

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 35;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 81 GGAGACATATGATAACCA 99
```

```
DB 1 GGAGACAUGAUAACCA 19

RESULT 74
US-11-101-244-1430755
; Sequence 1430755, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430755
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430755

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 35;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 497 TCAAAGGCATCCCTGTGTA 515
DB 1 UCAAAGGCAUCCUGUGUA 19

RESULT 75
US-11-101-244-1430756
; Sequence 1430756, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430756
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430756

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 52.6%; Pred. No. 35;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1655 GCTGATGTTCTGTATCTTA 1673
```

D_b 1 GCUGAUGUUCUGUAUCUUA 19

RESULT 76

```

US-11-101-244-1430757
; Sequence 1430757, Application US/110101244
; Publication No. US20050246794A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
;
; TITLE OF INVENTION: Functional and Hyper
;
; FILE REFERENCE: 13499US
;
; CURRENT APPLICATION NUMBER: US/11/101.244
;
; CURRENT FILING DATE: 2005-04-07
;
; PRIOR APPLICATION NUMBER: 60/502,050
;
; PRIOR FILING DATE: 2003-09-10
;
; PRIOR APPLICATION NUMBER: 60/426,137
;
; PRIOR FILING DATE: 2002-11-14
;
; NUMBER OF SEQ ID NOS: 1591911
;
; SOFTWARE: Proprietary
;
; SEQ ID NO 1430757
;
; LENGTH: 19
;
; TYPE: RNA
;
; ORGANISM: Homo sapiens
;
US-11-101-244-1430757

```

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 35;
Matches 15; Conservative 4; Mismatches 0; Indels

Qy 767 TCGATGAGCTGGCCCAAGTG 785
:|:|:|:|:|:|:|:|:|
Db 1 UCGAUGAGCTUGGCCCAAGUG 19

RESULT 77

```

US-11-101-244-1430758
; Sequence 1430758, Application US/110101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyper
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430758
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430758

```

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 35;
Matches 15; Conservative 4; Mismatches 0; Indels

Qy 1455 CATGAAAGTAAGGAGTTA 1473
||:|||||:|||||:|
pb 1 CAUGGAAAGUAAGGAGUUA 19

RESULT 78

```

US-11-101-244-1430759
; Sequence 1430759, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134950S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430759
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430759

```

```

Query Match          1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 35;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

Qy 808 GAGAAGACCAGTAAGATCT 826
|||||:|:|:|:
D'b 1 GAGAAGACCAGTAAGAUCT 19

RESULT 79

```

US-11-101-244-1430760
; Sequence 1430760, Application US/11101244
; Publication No. US20050246794A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
;
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;
; FILE REFERENCE: 134990S
;
; CURRENT APPLICATION NUMBER: US/11/101,244
;
; PRIOR FILING DATE: 2005-04-07
;
; PRIOR APPLICATION NUMBER: 60/502,050
;
; PRIOR FILING DATE: 2003-09-10
;
; PRIOR APPLICATION NUMBER: 60/426,137
;
; PRIOR FILING DATE: 2002-11-14
;
; NUMBER OF SEQ ID NOS: 1591911
;
; SOFTWARE: Proprietary
;
; SEQ ID NO 1430760
;
; LENGTH: 19
;
; TYPE: RNA
;
; ORGANISM: Homo sapiens
;
US-11-101-244-1430760

```

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 35;
Matches 14; Conservative 5; Mismatches 0; Indels

Qy 1678 GACCACAGTTTGTAA GTAC 1696
Db 1 GACCACAGUUUGUAAGUAC 19


```
US-11-101-244-1430765
; Sequence 1430765, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430765
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430765

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 68.4%; Pred. No. 35;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1677 TGACCACAGTTTCTGAAGTA 1695
Db 1 UGACCACAGUUUGUAGUA 19

RESULT 85
US-11-101-244-1430766
; Sequence 1430766, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430766
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430766

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 52.6%; Pred. No. 35;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1648 GTTCTTGGCTGATGTTCTG 1666
Db 1 GUUCUUGGCGUGAUGUUCUG 19

RESULT 86
US-11-101-244-1430767
; Sequence 1430767, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430767
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430767

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 35;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1524 TAACCAATCATGCAAACTT 1542
Db 1 UAACCAAUCAUGCAAACTU 19

RESULT 87
US-11-101-244-1430768
; Sequence 1430768, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430768
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430768

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 57.9%; Pred. No. 35;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1615 CCCACTCTATGTTATGTGA 1633
Db 1 CCCACUUAUGUUAUGUA 19

RESULT 88
US-11-101-244-1430769
; Sequence 1430769, Application US/11101244
```

RESULT 92
US-11-101-244-1430773
; Sequence 1430773, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:


```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430773
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430773
```

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 35;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
QY 1279 GGAGAGGCTTAGACCTGAA 1297
      |||||:::|||||
Db 1 GGAGAGGCUUAGACCUGAA 19
```

```
RESULT 93
US-11-101-244-1430774
; Sequence 1430774, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430774
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430774
```

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 35;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
QY 829 GACCTTATCAGCAGCATCA 847
      |||||:::|||||
Db 1 GACCUUAGCAGCAUCA 19
```

```
RESULT 94
US-11-101-244-1430775
; Sequence 1430775, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
```

```
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430775
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430775
```

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 52.6%; Pred. No. 35;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

```
QY 1656 CTGATGTTCTGTATCTTAA 1674
      |||||:::|||||
Db 1 CUGAUGUUCUGAUCUAA 19
```

```
RESULT 95
US-11-101-244-1430776
; Sequence 1430776, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430776
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430776
```

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 35;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
QY 1235 AAGCATGGCCTACAGAATG 1253
      |||||:::|||||
Db 1 AAGCAUGGCCUACAGNAUG 19
```

```
RESULT 96
US-11-101-244-1430777
; Sequence 1430777, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
```

```
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430777
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430777

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 52.6%; Pred. No. 35;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1635 GGAGTTGGTTCGTGGTCTTT 1653
Db 1 GGAGUUGGUUCUGGUUCUU 19

RESULT 97
US-11-101-244-1430778
; Sequence 1430778, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430778
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430778

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 89.5%; Pred. No. 35;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 141 CAAGGACCCCTGGCCACCAT 159
Db 1 CAAGGACCCUGGCCACCAU 19

RESULT 98
US-11-101-244-1430780
; Sequence 1430780, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430781
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430781

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 35;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1609 GCAGGGCCCACTCTATGTT 1627
Db 1 GCAGGGCCCAUCUUAUGUU 19

RESULT 99
US-11-101-244-1430781
; Sequence 1430781, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430781
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430781

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 63.2%; Pred. No. 35;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 168 GACATACCTTCATCTCT 186
Db 1 GAGCAUUAUCCUUAUCUCU 19

RESULT 100
US-11-101-244-1430782
; Sequence 1430782, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430782
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430782

```

```

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 35;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1447  GGCCTGATCATGGAAAGTA 1465
          |||:|:|:|:|:|:|:|:|:|
Db       1  GGCCUGAUGGAAAGUA 19

```

Search completed: March 11, 2006, 21:14:34
Job time : 685 secs